

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:05:38 ; Search time 232 Seconds
(without alignments)
408.258 Million cell updates/sec

Title: US-09-888-164-29
Perfect score: 16
Sequence: 1 aaagccacccaagca 16

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: N_Geneseq_16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	16	2	AAT18256
2	16	100.0	16	2	AAV14125
3	16	100.0	16	10	ADB68575
4	16	100.0	17	8	ACD55710
5	16	100.0	17	8	ACD55710
6	16	100.0	17	12	ADM59621
7	16	100.0	17	12	ADM60244
8	16	100.0	18	2	AAT71786
9	16	100.0	18	2	AAV14133
10	16	100.0	19	2	AAT71785
11	16	100.0	19	2	AAT71789
12	16	100.0	19	11	ADM00160
13	16	100.0	19	11	ADM00806
14	16	100.0	19	11	ADM00807
15	16	100.0	19	11	ADM00804
16	16	100.0	19	11	ADM00804
17	16	100.0	19	11	ADM00804
18	16	100.0	19	11	ADM00161
19	16	100.0	19	11	ADM00158
20	16	100.0	20	2	AAQ13771

C	21	16	100.0	20	2	AAQ13772
C	22	16	100.0	20	2	AAQ85970
C	23	16	100.0	20	2	AAT70947
C	24	16	100.0	21	2	AAQ32909
C	25	16	100.0	21	2	AAT18255
C	26	16	100.0	21	2	AAT18253
C	27	16	100.0	21	2	AAT70936
C	28	16	100.0	21	9	ADA13842
C	29	16	100.0	21	11	ADM00924
C	30	16	100.0	23	2	AAQ13770
C	31	16	100.0	23	2	AAT03266
C	32	16	100.0	23	2	AAQ81424
C	33	16	100.0	23	4	AAQ19005
C	34	16	100.0	23	11	ADM00880
C	35	16	100.0	30	2	AAV29303
C	36	16	100.0	32	4	AAQ14628
C	37	16	100.0	44	2	AAT71784
C	38	16	100.0	44	2	AAT71783
C	39	16	100.0	48	3	ABK14696
C	40	16	100.0	48	3	ABK14696
C	41	16	100.0	50	2	AAQ81436
C	42	16	100.0	54	3	AAQ24421
C	43	16	100.0	61	3	ABK14697
C	44	16	100.0	61	9	ACA62424
C	45	16	100.0	70	2	AAQ28267
C	46	16	100.0	72	2	AAT58386
C	47	16	100.0	87	2	AAT05545
C	48	16	100.0	87	4	AAQ09094
C	49	16	100.0	94	2	AAT73890
C	50	16	100.0	94	2	AAT73887
C	51	16	100.0	94	2	AAT73889
C	52	16	100.0	94	2	AAT73888
C	53	16	100.0	114	2	AAQ25403
C	54	16	100.0	129	4	AAQ09093
C	55	16	100.0	137	2	AAQ34316
C	56	16	100.0	291	2	AAQ25406
C	57	16	100.0	299	13	ADP79740
C	58	16	100.0	330	2	AAQ25411
C	59	16	100.0	534	2	AAQ25399
C	60	16	100.0	534	2	AAQ25400
C	61	16	100.0	534	2	AAT05543
C	62	16	100.0	560	10	AAT23617
C	63	16	100.0	560	10	ABT23618
C	64	16	100.0	560	12	ADN00634
C	65	16	100.0	588	2	AAQ25640
C	66	16	100.0	639	6	AAQ27422
C	67	16	100.0	639	6	AAQ31508
C	68	16	100.0	646	12	ADL56756
C	69	16	100.0	655	2	AAQ47014
C	70	16	100.0	655	2	AAT35649
C	71	16	100.0	655	4	AAH77569
C	72	16	100.0	655	4	AAH77568
C	73	16	100.0	655	4	AAH77574
C	74	16	100.0	655	4	AAH77573
C	75	16	100.0	655	4	AAH77570
C	76	16	100.0	655	4	AAH77571
C	77	16	100.0	655	4	AAQ21244
C	78	16	100.0	655	9	ABX80077
C	79	16	100.0	655	10	ABX96938
C	80	16	100.0	660	1	AAQ1081
C	81	16	100.0	663	3	AAQ1734
C	82	16	100.0	664	4	AAH77572
C	83	16	100.0	669	12	ADQ07220
C	84	16	100.0	673	4	AAQ09092
C	85	16	100.0	675	4	AAH77563
C	86	16	100.0	681	4	AAH77566
C	87	16	100.0	681	4	AAH77567
C	88	16	100.0	750	1	AAQ80943
C	89	16	100.0	909	6	AAH77169
C	90	16	100.0	1334	2	AAV82691
C	91	16	100.0	1395	2	AAV82688
C	92	16	100.0	1400	2	AAV82687
C	93	16	100.0	1445	2	AAV82692

AAQ13772	HBV prime
AaQ85970	Hepatitis
AaT70947	HBV pre-g
AaQ32909	Antiviral
AaT18255	HBV epsil
AaT18253	HBV epsil
AaT70936	HBV core
ADA13842	Short int
ADM00924	Hepatitis
AAQ13770	HBV prime
AaT03266	Hepatitis
AAQ81424	HBV hypoxi
AaD19005	Hepatitis
ADM00880	Hepatitis
AAV29303	Hepatitis
AAQ14628	NASBA mol
AaT71784	Hepatitis
AaT71783	Hepatitis
ABK14696	HBV encap
ABK14696	RNA targ
AAQ81436	HBV targ
AAQ24421	Hepatitis
ABK14697	HBV prege
ACA62424	Hepatitis
AAQ28267	Sequence
AaT58386	Hepatitis
AaT05545	Human hep
AAQ09094	Hepatitis
AAT73890	Human hep
AAT73887	Human hep
AaT73889	Human hep
AaT73888	Human hep
AaQ25403	Sequence
AAQ09093	Hepatitis
AaX34316	Fragment
ADP79740	Sequence
AaQ25411	Sequence
AAQ25399	Sequence
AaQ25400	HBV core
AAT05543	Human hep
ABT23617	Stabiliser
ABT23618	Stabiliser
ADN00634	Hepatitis
AaQ25640	Sequence
AaQ27422	Hepatitis
AaQ31508	Hepatitis
ADL56756	HBV prece
AaQ47014	HBV (adv)
AaT35649	Precore/c
AaH77569	HBV genot
AaH77568	HBV genot
AaH77574	HBV genot
AaH77573	HBV genot
AaH77570	HBV genot
AaH77571	HBV genot
AaQ21244	Hepatitis
ABX80077	Hepatitis
ABX96938	Hepatitis
AAQ1081	DNA beque
AaA71734	HBV fusio
AaH77572	HBV genot
ADQ07220	Hepatitis
AAQ09092	Hepatitis
AAH77563	HBV prece
AAH77566	HBV genot
AAH77567	HBV genot
AaA80943	HBV core
AaH77169	Regulator
AaV82691	Fulminant
AaV82688	Fulminant
AaV82687	Fulminant
AaV82692	Fulminant

C 94	16	100.0	1445	2	AAV82685	AAV82685	Fulminant	C 167	15	93.8	30	6	ABL50306	ABL50306	Hepatitis
C 95	16	100.0	1445	2	AAV82690	AAV82690	Fulminant	C 168	15	93.8	644	3	AAFI4461	AAFI4461	Hepatitis
C 96	16	100.0	1445	2	AAV82684	AAV82684	Fulminant	C 169	15	93.8	696	9	ADAS0189	ADAS0189	Human CDN
C 97	16	100.0	1500	2	AAV82685	AAV82685	Fulminant	C 170	15	93.8	864	9	ABTI9286	ABTI9286	Hepatitis
C 98	16	100.0	1500	2	AAV82683	AAV82683	Fulminant	C 171	15	93.8	864	8	ABTI1106	ABTI1106	Hepatitis
C 99	16	100.0	1500	2	AAV82694	AAV82694	Fulminant	C 172	15	93.8	1041	8	ABTI1862	ABTI1862	Hepatitis
C 100	16	100.0	1500	2	AAV82697	AAV82697	Fulminant	C 173	15	93.8	1041	8	ABTI2058	ABTI2058	Hepatitis
C 101	16	100.0	1500	2	AAV82686	AAV82686	Fulminant	C 174	15	93.8	1591	5	AA686799	AA686799	DNA encod
C 102	16	100.0	1500	2	AAV82706	AAV82706	Fulminant	C 175	15	93.8	1921	5	AA683448	AA683448	DNA encod
C 103	16	100.0	1500	2	AAV82689	AAV82689	Fulminant	C 176	15	93.8	3041	8	ABTI1912	ABTI1912	Hepatitis
C 104	16	100.0	1500	2	AAV82593	AAV82593	Fulminant	C 177	15	93.8	3041	8	ABTI18098	ABTI18098	Hepatitis
C 105	16	100.0	1500	2	AAV82696	AAV82696	Fulminant	C 178	15	93.8	3215	6	ABIS5204	ABIS5204	Hepatitis
C 106	16	100.0	1503	2	AAV82596	AAV82596	Fulminant	C 179	15	93.8	4682	12	AD086465	AD086465	Hepatitis
C 107	16	100.0	1977	12	ADJ53703	ADJ53703	RNA pseud	C 180	15	93.8	4682	13	ACN39455	ACN39455	Hepatitis
C 108	16	100.0	2342	1	AAV93072	AAV93072	Sequence	C 181	15	93.8	4692	10	AD673109	AD673109	Hepatitis
C 109	16	100.0	2743	1	AAV93072	AAV93072	Sequence	C 182	15	93.8	4692	13	AD673109	AD673109	Hepatitis
C 110	16	100.0	2743	1	AAV93072	AAV93072	Sequence	C 183	15	93.8	4896	4	AAI59468	AAI59468	Hepatitis
C 111	16	100.0	3180	4	AAH42375	AAH42375	Sequence	C 184	15	93.8	4944	12	ADP75923	ADP75923	Hepatitis
C 112	16	100.0	3182	6	AAH42375	AAH42375	Sequence	C 185	15	93.8	4944	12	ADP75923	ADP75923	Hepatitis
C 113	16	100.0	3182	6	AAH42375	AAH42375	Sequence	C 186	15	93.8	4944	12	ADP75923	ADP75923	Hepatitis
C 114	16	100.0	3182	6	AAH42375	AAH42375	Sequence	C 187	15	93.8	4944	12	ADP75923	ADP75923	Hepatitis
C 115	16	100.0	3182	6	AAH42375	AAH42375	Sequence	C 188	15	93.8	4944	12	ADP75923	ADP75923	Hepatitis
C 116	16	100.0	3182	6	AAH42375	AAH42375	Sequence	C 189	15	93.8	4944	12	ADP75923	ADP75923	Hepatitis
C 117	16	100.0	3188	9	AAV30035	AAV30035	Hepatitis	C 190	15	93.8	48133	11	ACN44860	ACN44860	Hepatitis
C 118	16	100.0	3188	12	ADP56973	ADP56973	Hepatitis	C 191	15	93.8	53021	11	ACN44860	ACN44860	Hepatitis
C 119	16	100.0	3188	12	ADP56973	ADP56973	Hepatitis	C 192	15	93.8	53021	11	ACN44860	ACN44860	Hepatitis
C 120	16	100.0	3192	2	AAV82685	AAV82685	Fulminant	C 193	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 121	16	100.0	3200	1	AAV82685	AAV82685	Fulminant	C 194	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 122	16	100.0	3200	1	AAV82685	AAV82685	Fulminant	C 195	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 123	16	100.0	3200	1	AAV82685	AAV82685	Fulminant	C 196	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 124	16	100.0	3214	1	AAV82685	AAV82685	Fulminant	C 197	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 125	16	100.0	3215	3	AAZ29453	AAZ29453	Mutant he	C 198	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 126	16	100.0	3215	3	AAZ29453	AAZ29453	Mutant he	C 199	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 127	16	100.0	3215	3	AAZ29453	AAZ29453	Mutant he	C 200	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 128	16	100.0	3215	11	ADN35114	ADN35114	Hepatitis	C 201	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 129	16	100.0	3221	12	ADN35114	ADN35114	Hepatitis	C 202	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 130	16	100.0	3221	4	AAH42374	AAH42374	Nucleotid	C 203	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 131	16	100.0	3221	6	ABK23902	ABK23902	Bea venom	C 204	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 132	16	100.0	3221	6	ABK23902	ABK23902	Bea venom	C 205	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 133	16	100.0	3221	6	ABK23902	ABK23902	Bea venom	C 206	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 134	16	100.0	3221	6	ABK23902	ABK23902	Bea venom	C 207	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 135	16	100.0	3221	10	ADN27773	ADN27773	Hepatitis	C 208	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 136	16	100.0	3221	13	ADN27773	ADN27773	Hepatitis	C 209	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 137	16	100.0	3221	13	ADN27773	ADN27773	Hepatitis	C 210	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 138	16	100.0	3248	4	AAV82685	AAV82685	Fulminant	C 211	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 139	16	100.0	3248	4	AAV82685	AAV82685	Fulminant	C 212	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 140	16	100.0	3835	2	AAV82685	AAV82685	Fulminant	C 213	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 141	16	100.0	4084	4	AAV82685	AAV82685	Fulminant	C 214	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 142	16	100.0	4421	2	AAV82685	AAV82685	Fulminant	C 215	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 143	16	100.0	4421	2	AAV82685	AAV82685	Fulminant	C 216	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 144	16	100.0	4839	4	ABL08429	ABL08429	Hepatitis	C 217	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 145	16	100.0	5037	12	ADJ27202	ADJ27202	Fruitfly	C 218	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 146	16	100.0	5618	2	AAV82685	AAV82685	Fulminant	C 219	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 147	16	100.0	5639	2	AAV82685	AAV82685	Fulminant	C 220	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 148	16	100.0	5676	13	ADN23292	ADN23292	Recombina	C 221	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 149	16	100.0	6371	2	AAZ23285	AAZ23285	DNA seque	C 222	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 150	16	100.0	6371	2	AAZ23285	AAZ23285	DNA seque	C 223	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 151	16	100.0	6942	4	AAV82685	AAV82685	Fulminant	C 224	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 152	16	100.0	7085	4	AAV82685	AAV82685	Fulminant	C 225	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 153	16	100.0	7991	6	AAV82685	AAV82685	Fulminant	C 226	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 154	16	100.0	8007	6	AAV82685	AAV82685	Fulminant	C 227	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 155	16	100.0	8717	6	AAV82685	AAV82685	Fulminant	C 228	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 156	16	100.0	9335	2	AAZ23282	AAZ23282	DNA seque	C 229	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 157	16	100.0	9534	2	AAZ23282	AAZ23282	DNA seque	C 230	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 158	16	100.0	9542	5	AAV82685	AAV82685	Fulminant	C 231	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 159	16	100.0	9542	5	AAV82685	AAV82685	Fulminant	C 232	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 160	16	100.0	9859	8	ABX3525	ABX3525	DNA encod	C 233	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 161	16	100.0	9859	8	ABX3525	ABX3525	DNA encod	C 234	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 162	15	93.8	16	8	AAV82685	AAV82685	Fulminant	C 235	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 163	15	93.8	17	12	ADN60043	ADN60043	Hepatitis	C 236	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 164	15	93.8	19	11	ADN99647	ADN99647	Hepatitis	C 237	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 165	15	93.8	19	11	ADN99647	ADN99647	Hepatitis	C 238	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis
C 166	15	93.8	20	2	AAV70948	AAV70948	HBV pre-g	C 239	15	93.8	227448	13	ABD32841	ABD32841	Hepatitis

C 240	14	87.5	2233	4	ABL17591	ABL17591 Drosophila	C 313	13	81.2	23	11	ADM00889	ADM00889 Hepatitis
241	14	87.5	3026	13	ADQ86001	Adq86001 Human tum	C 314	13	81.2	27	2	AAT05554	Aat05554 Human hep
242	14	87.5	3026	13	ADQ87475	Adq87475 Human tum	C 315	13	81.2	30	2	AAO74959	Aao74959 Hepatitis
243	14	87.5	3034	6	ABK83882	Abk83882 Human CDN	C 316	13	81.2	30	2	AAO74960	Aao74960 Hepatitis
244	14	87.5	3034	6	ABZ71983	Abz71983 Human pho	C 317	13	81.2	34	2	AAO47022	Aao47022 HBV preco
C 245	14	87.5	3150	4	ABL18734	AbL18734 Drosophila	C 318	13	81.2	34	2	AAO86218	Aao86218 HBV adw b
C 246	14	87.5	3274	4	ABL18736	AbL18736 Drosophila	C 319	13	81.2	34	2	AAT35660	Aat35660 Primer #3
247	14	87.5	3452	12	ADM79336	Adm79336 Mouse 1ym	C 320	13	81.2	34	2	AAT31174	Aat31174 XhoI site
248	14	87.5	3454	6	AAD41009	Aad41009 Mouse P13	C 321	13	81.2	34	2	AAV42249	Aav42249 PCR prime
249	14	87.5	3454	6	ABK72319	Abk72319 DNA encod	C 322	13	81.2	34	2	AAV62008	Aav62008 Sense PCR
250	14	87.5	3454	6	ABK72292	Abk72292 Lymphona	C 323	13	81.2	34	2	AAV30014	Aav30014 PCR prime
251	14	87.5	3454	6	ABSS4198	Abss4198 Mouse CDN	C 324	13	81.2	34	2	AAV70769	Aav70769 PCR prime
252	14	87.5	3454	9	ADA02928	Ada02928 Mouse P1k	C 325	13	81.2	34	3	AAZ29293	Aaz29293 HBV core
253	14	87.5	3454	10	ADB72666	Adb72666 Mouse P1k	C 326	13	81.2	34	3	AAZ29286	Aaz29286 HBV core
254	14	87.5	3454	10	ADC85408	Adc85408 Mouse P1k	C 327	13	81.2	34	4	AAZ29195	Aaz29195 Sense PCR
255	14	87.5	3454	12	ADM79337	Adm79337 Mouse 1ym	C 328	13	81.2	34	6	AAI38873	Aai38873 Alphaviru
256	14	87.5	3454	12	ADM74523	Adm74523 Murine ca	C 329	13	81.2	34	6	ABK46339	Abk46339 HBV core
257	14	87.5	3454	12	ADQ60051	Adq60051 C6H sigma	C 330	13	81.2	34	9	ABX80029	Abx80029 Hepatitis
258	14	87.5	3523	6	ABQ54610	Abq54610 Mouse ova	C 331	13	81.2	34	10	ABX96890	Abx96890 Hepatitis
259	14	87.5	3633	2	AAT97611	Aat97611 Mouse E2A	C 332	13	81.2	34	12	ADL30446	Adl30446 HBV core
260	14	87.5	3728	2	AAQ58708	Aaq58708 Mouse OSF	C 333	13	81.2	34	12	ADL56744	Adl56744 HBV core
261	14	87.5	3854	2	AAT97610	Aat97610 Human E2A	C 334	13	81.2	34	12	ADL14005	Adl14005 Burkayoti
262	14	87.5	3872	10	ADER9063	Der9063 Human pro	C 335	13	81.2	80	12	ADM96072	Adm96072 Rat anti
263	14	87.5	3914	12	ADQ86121	Adq86121 Human tum	C 336	13	81.2	94	2	AAT73892	Aat73892 Human hep
264	14	87.5	3914	13	ACN38620	Acn38620 Tumour-t8	C 337	13	81.2	94	2	AAT73891	Aat73891 Human hep
265	14	87.5	3922	9	ACH03928	Ach03928 Human CDN	C 338	13	81.2	141	2	AAT69055	Aat69055 Hepatitis
266	14	87.5	3935	8	ABZ34770	Abz34770 Coding se	C 339	13	81.2	207	5	AAH67687	Aah67687 C glutami
267	14	87.5	3935	8	ACC50076	Acc50076 Breast ca	C 340	13	81.2	228	12	ACH93965	Ach93965 Human gen
268	14	87.5	3935	10	ADP90653	Adp90653 Human hep	C 341	13	81.2	231	8	ACA01159	Acca01159 C. glutam
269	14	87.5	4025	10	ADER9067	Der9067 Human pro	C 342	13	81.2	231	12	ADQ21864	Adq21864 Human bof
270	14	87.5	4125	13	ADRA4022	Adra4022 Human col	C 343	13	81.2	240	2	AAH86378	Aah86378 Human sin
271	14	87.5	4233	1	ABL17590	AbL17590 Drosophila	C 344	13	81.2	240	2	AAH86380	Aah86380 Human sin
272	14	87.5	4236	8	ACA39046	AcA39046 Prokaryot	C 345	13	81.2	240	4	AAI23709	Aai23709 Probe #13
273	14	87.5	4259	12	ADL03415	AdL03415 DNA encod	C 346	13	81.2	240	4	ABA68824	AbA68824 Human flo
274	14	87.5	4483	4	ABL07558	AbL07558 Drosophila	C 347	13	81.2	240	4	AAI49022	Aai49022 Probe #17
C 275	14	87.5	5533	3	AAC63529	Aac63529 Silt prot	C 348	13	81.2	240	4	ABA50851	AbA50851 Human bre
C 276	14	87.5	6391	13	ADQ85331	Adq85331 Human tum	C 349	13	81.2	240	4	ABA53777	AbA53777 Probe #14
277	14	87.5	6627	5	AAH86211	Aah86211 Human DNA	C 350	13	81.2	240	4	AAK42945	Aak42945 Human bon
278	14	87.5	6627	5	AAH86211	Aah86211 DNA encod	C 351	13	81.2	240	4	AAK17160	Aak17160 Human bra
279	14	87.5	6981	13	ACNA42918	Acna42918 Human dia	C 352	13	81.2	240	4	ABSA42577	AbSA42577 Human liv
280	14	87.5	6997	13	ACNA42917	Acna42917 Human dia	C 353	13	81.2	240	5	AAI09326	Aai09326 Probe #93
281	14	87.5	7697	9	ACD28255	AcD28255 Mouse bof	C 354	13	81.2	240	6	ABSI1707	AbSI1707 Human gen
282	14	87.5	10558	4	ABL02846	AbL02846 Drosophila	C 355	13	81.2	243	10	ADH84063	Adh84063 Enterococ
283	14	87.5	13104	2	AAQ46852	Aaq46852 Clone of	C 356	13	81.2	282	13	ADR91549	Adr91549 Novel S.
C 284	14	87.5	16161	6	AAAD36071	AaD36071 Human adi	C 357	13	81.2	289	13	ADR29684	Adr29684 Mouse gen
285	14	87.5	18737	4	ABL07492	AbL07492 Drosophila	C 358	13	81.2	300	2	AAZ14607	Aaz14607 Human gen
286	14	87.5	18737	4	ABL07530	AbL07530 Drosophila	C 359	13	81.2	308	13	ADR93088	Adr93088 Novel S.
287	14	87.5	31063	4	AAF28533	Aaf28533 Genomic f	C 360	13	81.2	339	12	ADQ18067	Adq18067 Human bof
C 288	14	87.5	43229	11	ACNA4192	Acna4192 Mouse gen	C 361	13	81.2	343	8	ABX42722	Abx42722 Bovine ES
289	14	87.5	53601	12	ADQ97749	Adq97749 Human can	C 362	13	81.2	365	8	ABZ37683	Abz37683 Porcine 5
290	14	87.5	80268	13	ABD32951	Abd32951 Mouse can	C 363	13	81.2	394	9	ACH25666	Ach25666 Human adu
291	14	87.5	80578	4	AAH44800	Aah44800 Human GPC	C 364	13	81.2	396	4	AAI81388	Aai81388 Human pol
292	14	87.5	92726	9	ADA02927	Ada02927 Mouse P1k	C 365	13	81.2	399	10	ADR81376	Adr81376 Leukemia
293	14	87.5	92726	10	ADR12665	Adr12665 Mouse P1k	C 366	13	81.2	401	9	AAI60864	Aai60864 Human CYP
294	14	87.5	92726	12	ADC85407	Adc85407 Mouse P1k	C 367	13	81.2	416	5	ABVE2019	Abve2019 Human pro
295	14	87.5	92726	12	ADM74522	Adm74522 Murine ca	C 368	13	81.2	416	5	ABVE2117	Abve2117 Human pro
C 296	14	87.5	100137	9	ADQ97643	AdQ97643 Human can	C 369	13	81.2	416	5	ABVE2176	Abve2176 Human pro
C 297	14	87.5	110000	12	ADQ97643	AdQ97643 Human can	C 370	13	81.2	416	5	ABVE1984	Abve1984 Human pro
C 298	14	87.5	122779	12	ADQ87053	AdQ87053 Mouse can	C 371	13	81.2	420	3	ADR57131	Adr57131 Urogenita
299	14	87.5	129017	12	ADP84158	Adp84158 Human AST	C 372	13	81.2	421	12	ADQ80746	Adq80746 Porcine e
C 300	14	87.5	162450	3	AAZ86967	Aaz86967 Retinobla	C 373	13	81.2	427	6	ABL82633	AbL82633 Human ova
C 301	13	81.2	15	8	ACD56186	AcD56186 HBV enzym	C 374	13	81.2	438	9	ACL20721	ACL20721 DNA clone
C 302	13	81.2	15	12	ADM63883	Adm63883 Hepatitis	C 375	13	81.2	440	13	ADQ53724	AdQ53724 Novel can
C 303	13	81.2	16	2	AAT18258	Aat18258 HBV epsil	C 376	13	81.2	444	6	ABR9498	AbR9498 Human CYP
C 304	13	81.2	17	8	ACD53523	AcD53523 HBV inozy	C 377	13	81.2	449	4	AAI14509	Aai14509 Probe #44
C 305	13	81.2	17	8	ACD53531	AcD53531 HBV ziny	C 378	13	81.2	449	4	ABA56240	AbA56240 Human f0e
C 306	13	81.2	17	12	ADM59622	Adm59622 Hepatitis	C 379	13	81.2	449	4	AAI35884	Aai35884 Probe #45
C 307	13	81.2	19	12	ADM59016	Adm59016 Hepatitis	C 380	13	81.2	449	4	ABA45731	AbA45731 Human bre
C 308	13	81.2	19	11	ADM00283	Adm00283 Hepatitis	C 381	13	81.2	449	4	ABA25880	AbA25880 Probe #43
C 309	13	81.2	20	11	ADL99636	Adl99636 Hepatitis	C 382	13	81.2	449	4	AAK29919	Aak29919 Human bon
C 310	13	81.2	20	2	AAO81425	Aao81425 HBV hybr	C 383	13	81.2	449	4	AAK04423	Aak04423 Human bra
C 311	13	81.2	21	2	AAT18257	Aat18257 HBV epsil	C 384	13	81.2	449	4	ABSS2958	Abss2958 Human liv
C 312	13	81.2	21	11	ADM00999	Adm00999 Hepatitis	C 385	13	81.2	449	5	AAI04334	Aai04334 Probe #43

386	13	81.2	449	6	ABSO4487	Abso4487 Human gen	C 459	13	81.2	628	9	ACL20732	ACL20732 DNA clone
387	13	81.2	454	9	ACH3437	ACH3437 Human end	C 460	13	81.2	629	9	ACL20743	ACL20743 DNA clone
C 388	13	81.2	456	10	ADK61537	ADK61537 Ovarian c	C 461	13	81.2	630	9	ACL20769	ACL20769 DNA clone
389	13	81.2	463	10	ABZ84631	ABZ84631 Toxicolog	C 462	13	81.2	634	9	ACL20773	ACL20773 DNA clone
390	13	81.2	464	4	AA111903	AA111903 Probe #18	C 463	13	81.2	637	9	ACL20708	ACL20708 DNA clone
391	13	81.2	464	4	ABAS3606	ABAS3606 Human foe	C 464	13	81.2	640	9	ACL20765	ACL20765 DNA clone
392	13	81.2	464	4	AA133233	AA133233 Probe #19	C 465	13	81.2	642	8	ACA39691	ACA39691 Prokaryot
393	13	81.2	464	4	ABAA3361	ABAA3361 Probe #18	C 466	13	81.2	644	9	ACL20697	ACL20697 DNA clone
394	13	81.2	464	4	AAK27329	AAK27329 Human don	C 467	13	81.2	645	9	ACL20698	ACL20698 DNA clone
395	13	81.2	464	4	AAK01872	AAK01872 Human bra	C 468	13	81.2	647	4	AAK63140	AAK63140 Human imm
396	13	81.2	464	4	ABSG26903	ABSG26903 Human bra	C 469	13	81.2	648	9	ACL20758	ACL20758 DNA clone
397	13	81.2	464	6	ABSO1849	ABSO1849 Human gen	C 470	13	81.2	653	2	AAV52491	AAV52491 Streptococ
C 398	13	81.2	469	5	ABV58365	ABV58365 Human pro	C 471	13	81.2	654	9	ACL20738	ACL20738 DNA clone
399	13	81.2	474	9	ACH41721	ACH41721 Human foe	C 472	13	81.2	658	9	ACL20745	ACL20745 DNA clone
400	13	81.2	478	9	ACH13859	ACH13859 Human adu	C 473	13	81.2	659	3	AAA51795	AAA51795 CASP8 DNA
C 401	13	81.2	485	13	ACN51896	ACN51896 Cotton an	C 474	13	81.2	660	9	ACL20699	ACL20699 DNA clone
C 402	13	81.2	487	13	ACN51896	ACN51896 Cotton an	C 475	13	81.2	664	9	ACL20760	ACL20760 DNA clone
C 403	13	81.2	492	9	ACL20696	ACL20696 DNA clone	C 476	13	81.2	671	9	ACL20768	ACL20768 DNA clone
C 404	13	81.2	492	9	ACL20695	ACL20695 DNA clone	C 477	13	81.2	674	9	ACL20719	ACL20719 DNA clone
C 405	13	81.2	493	10	ADB55993	ADB55993 Toxicity-	C 478	13	81.2	681	10	ABX07776	ABX07776 S. pneumo
C 406	13	81.2	498	9	ACH24092	ACH24092 Human adu	C 479	13	81.2	682	9	ACL20766	ACL20766 DNA clone
C 407	13	81.2	501	9	ACH41422	ACH41422 Human foe	C 480	13	81.2	687	9	ACL20714	ACL20714 DNA clone
C 408	13	81.2	503	9	ACH41422	ACH41422 Human foe	C 481	13	81.2	687	9	ACL20694	ACL20694 DNA clone
C 409	13	81.2	505	9	ACL20720	ACL20720 DNA clone	C 482	13	81.2	688	9	ACL20715	ACL20715 DNA clone
C 410	13	81.2	509	9	ACL20716	ACL20716 DNA clone	C 483	13	81.2	690	9	ACL20723	ACL20723 DNA clone
C 411	13	81.2	519	13	ACN58104	ACN58104 Cotton gy	C 484	13	81.2	692	9	ACL20706	ACL20706 DNA clone
C 412	13	81.2	524	9	ACL20733	ACL20733 DNA clone	C 485	13	81.2	694	9	ACL20729	ACL20729 DNA clone
C 413	13	81.2	526	13	ACN58123	ACN58123 Cotton gy	C 486	13	81.2	700	9	ACL20718	ACL20718 DNA clone
C 414	13	81.2	536	9	ACL20750	ACL20750 DNA clone	C 487	13	81.2	707	9	ACL20705	ACL20705 DNA clone
C 415	13	81.2	537	12	ACH80265	ACH80265 Human gen	C 488	13	81.2	709	9	ACL20726	ACL20726 DNA clone
C 416	13	81.2	539	3	AAPO9493	AAPO9493 Fusarium	C 489	13	81.2	718	10	ADF82745	ADF82745 Leukemia
C 417	13	81.2	542	9	ACL20702	ACL20702 DNA clone	C 490	13	81.2	722	9	ACL20724	ACL20724 DNA clone
C 418	13	81.2	542	9	ACL20746	ACL20746 DNA clone	C 491	13	81.2	725	4	AAH34565	AAH34565 Human col
C 419	13	81.2	542	9	ACL20761	ACL20761 DNA clone	C 492	13	81.2	729	12	ADU43417	ADU43417 Plant cDN
C 420	13	81.2	543	13	ADS34562	ADS34562 POSH prot	C 493	13	81.2	735	12	ADU43418	ADU43418 Plant cDN
C 421	13	81.2	545	9	ACL20749	ACL20749 DNA clone	C 494	13	81.2	741	10	ADU34290	ADU34290 Mouse mit
C 422	13	81.2	547	9	ACL20707	ACL20707 DNA clone	C 495	13	81.2	762	5	AAST0070	AAST0070 DNA encod
C 423	13	81.2	553	9	ACL20710	ACL20710 DNA clone	C 496	13	81.2	765	4	AAAL16187	AAAL16187 Human bre
C 424	13	81.2	553	9	ACL20764	ACL20764 DNA clone	C 497	13	81.2	786	4	AAAL25030	AAAL25030 Human bre
C 425	13	81.2	553	9	ACL20727	ACL20727 DNA clone	C 498	13	81.2	886	4	AAH66472	AAH66472 Streptococ
C 426	13	81.2	554	9	ACL20735	ACL20735 DNA clone	C 499	13	81.2	912	6	ABT44092	ABT44092 Streptococ
C 427	13	81.2	558	9	ACL20736	ACL20736 DNA clone	C 500	13	81.2	912	11	ADJ12093	ADJ12093 Plant cDN
C 428	13	81.2	558	9	ACL20752	ACL20752 DNA clone	C 501	13	81.2	912	12	ADU44593	ADU44593 Plant cDN
C 429	13	81.2	565	13	ACN48458	ACN48458 Cotton pr	C 502	13	81.2	915	8	ACA50774	ACA50774 Prokaryot
C 430	13	81.2	567	13	ACN59156	ACN59156 Cotton gy	C 503	13	81.2	915	12	ADT42917	ADT42917 Plant tra
C 431	13	81.2	568	9	ACL20722	ACL20722 DNA clone	C 504	13	81.2	931	6	ABT94986	ABT94986 Mouse isc
C 432	13	81.2	574	9	ACL20717	ACL20717 DNA clone	C 505	13	81.2	933	6	AAH69276	AAH69276 Human cer
C 433	13	81.2	581	9	ACL20756	ACL20756 DNA clone	C 506	13	81.2	935	4	AAH67643	AAH67643 C. glutami
C 434	13	81.2	582	9	ACL20762	ACL20762 DNA clone	C 507	13	81.2	937	12	ADO80705	ADO80705 Porcine e
C 435	13	81.2	584	9	ACL20753	ACL20753 DNA clone	C 508	13	81.2	939	8	ACA01119	ACA01119 C. glutami
C 436	13	81.2	585	9	ACL20747	ACL20747 DNA clone	C 509	13	81.2	978	13	ACN38711	ACN38711 Tumour-as
C 437	13	81.2	586	9	ACL20730	ACL20730 DNA clone	C 510	13	81.2	978	13	ACN34563	ACN34563 Breast ca
C 438	13	81.2	587	13	ACN58034	ACN58034 Cotton gy	C 511	13	81.2	983	11	ACN86135	ACN86135 Breast ca
C 439	13	81.2	588	9	ACL20731	ACL20731 DNA clone	C 512	13	81.2	983	11	ADT85500	ADT85500 Aspergill1
C 440	13	81.2	590	9	ACL20725	ACL20725 DNA clone	C 513	13	81.2	990	13	ABAA1614	ABAA1614 Human ner
C 441	13	81.2	590	9	ACL20737	ACL20737 DNA clone	C 514	13	81.2	996	6	ABL69980	ABL69980 Pancreas
C 442	13	81.2	592	13	ACN53574	ACN53574 Cotton an	C 515	13	81.2	996	6	ABR84035	ABR84035 Human cDN
C 443	13	81.2	594	6	ABR99424	ABR99424 Human CYP	C 516	13	81.2	996	6	ABR84035	ABR84035 Human cDN
C 444	13	81.2	594	6	ABR99426	ABR99426 Human CYP	C 517	13	81.2	996	13	ADT34559	ADT34559 POSH prot
C 445	13	81.2	594	6	ABR99425	ABR99425 Human CYP	C 518	13	81.2	999	13	ADT34561	ADT34561 POSH prot
C 446	13	81.2	601	6	ABR99427	ABR99427 Human CYP	C 519	13	81.2	1003	13	ADT61210	ADT61210 Bacterial
C 447	13	81.2	605	9	ACL20700	ACL20700 Human CYP	C 520	13	81.2	1058	10	ADT58512	ADT58512 Toxicity-
C 448	13	81.2	608	13	ACL20741	ACL20741 DNA clone	C 521	13	81.2	1066	6	ADT53116	ADT53116 Primary r
C 449	13	81.2	608	13	ACN58014	ACN58014 Cotton gy	C 522	13	81.2	1066	6	ADT34560	ADT34560 POSH prot
C 450	13	81.2	612	9	ACL20763	ACL20763 DNA clone	C 523	13	81.2	1083	3	AAAP1796	AAAP1796 Methyloph
C 451	13	81.2	612	13	ADT93335	ADT93335 Novel S.	C 524	13	81.2	1095	3	ADT47908	ADT47908 Bacterial
C 452	13	81.2	613	13	ADT93335	ADT93335 Novel S.	C 525	13	81.2	1110	13	ABX94959	ABX94959 Rice RacB
C 453	13	81.2	614	9	ACL20739	ACL20739 DNA clone	C 526	13	81.2	1113	8	ACA26126	ACA26126 Prokaryot
C 454	13	81.2	614	9	ACL20703	ACL20703 DNA clone	C 527	13	81.2	1184	13	ADT93947	ADT93947 Novel S.
C 455	13	81.2	621	9	ACL20751	ACL20751 DNA clone	C 528	13	81.2	1215	9	ADA31441	ADA31441 DNA encod
C 456	13	81.2	622	2	AAK30872	AAK30872 Streptococ	C 529	13	81.2	1229	4	AAK31608	AAK31608 CDNA enco
C 457	13	81.2	624	9	ACL20709	ACL20709 DNA clone	C 530	13	81.2	1250	10	AAH56257	AAH56257 Murine PE
C 458	13	81.2	626	9	ACL20742	ACL20742 DNA clone	C 531	13	81.2	1250	10	AAH56257	AAH56257 Murine PE

532	13	81.2	1254	8	ADA70016	Ada70016 Rice gene	C 605	13	81.2	3411	10	ADF81485	Adf81485 Leukemia
533	13	81.2	1317	10	ADF58610	Adf58610 Human pol	C 606	13	81.2	3411	12	ADQ84407	Adq84407 Human tum
534	13	81.2	1342	4	AAS33102	Aas33102 DNA encod	C 607	13	81.2	3411	12	ADQ83932	Adq83932 Human tum
535	13	81.2	1344	6	ABZ17335	Abz17335 Arabidops	C 608	13	81.2	3411	13	ADQ85162	Adq85162 Human tum
536	13	81.2	1381	6	ABK84318	Abk84318 Human CDN	C 609	13	81.2	3411	13	ADQ86341	Adq86341 Human tum
537	13	81.2	1381	10	ADD29828	Add29828 Human tum	C 610	13	81.2	3411	13	ADQ83255	Adq83255 Human tum
538	13	81.2	1381	13	ADR25263	Adr25263 Breast ca	C 611	13	81.2	3411	13	ACN37510	Acn37510 Tumour-ab
539	13	81.2	1395	13	ADP23501	Adp23501 PRO POLYp	C 612	13	81.2	3411	13	ACN37510	Acn37510 Tumour-ab
540	13	81.2	1404	13	AD548622	Ad548622 Bacterial	C 613	13	81.2	3411	13	ACN37510	Acn37510 Tumour-ab
541	13	81.2	1447	4	ABLO8661	Ablo8661 Drosophi1	C 614	13	81.2	3411	3	AAA40241	Aaa40241 Pig heart
542	13	81.2	1471	12	AD142017	Ad142017 Plant tra	C 615	13	81.2	3411	11	ADM01816	Adm01816 Human CDN
543	13	81.2	1471	12	AD002568	Ad002568 Soybean c	C 616	13	81.2	3411	6	ABA96529	Ab96529 G protein
544	13	81.2	1471	12	AD062205	Ad062205 Transcrip	C 617	13	81.2	3411	10	ADBS8084	Adbs8084 Toxicity- r
545	13	81.2	1497	4	ABL09123	Ablo9123 Drosophi1	C 618	13	81.2	3411	4	ADBS2562	Adbs2562 Primary r
546	13	81.2	1518	13	ADT44191	Adt44191 Bacteri1	C 619	13	81.2	3411	4	ABL09122	Ablo9122 Drosophi1
547	13	81.2	1525	6	ABN97321	Abn97321 Gene #381	C 620	13	81.2	3411	12	ADQ95194	Adq95194 Human sof
548	13	81.2	1539	6	AAS33301	Aas33301 DNA encod	C 621	13	81.2	3411	6	ABE67757	Ab67757 Human int
549	13	81.2	1572	10	AD883553	Ad883553 Human gen	C 622	13	81.2	3411	12	ADOT7132	Adot7132 Human BTL
550	13	81.2	1587	6	AAD44510	Aad44510 A. variab	C 623	13	81.2	3411	6	ABO79664	Abot79684 DNA seque
551	13	81.2	1599	11	AD132079	Ad132079 Human CDN	C 624	13	81.2	3411	10	AD050062	Ad050062 Human fat
552	13	81.2	1613	4	AAH17591	Aah17591 Human CDN	C 625	13	81.2	3411	11	ADOT7948	Adot7948 Brascica
553	13	81.2	1629	11	AD131202	Ad131202 Human CDN	C 626	13	81.2	3411	4	ACB91702	Ac91702 Mouse fat
554	13	81.2	1677	10	ADC08124	Adc08124 Rice DNA	C 627	13	81.2	3411	10	ABX08985	Abx08985 CDNA enc
555	13	81.2	1686	10	ADF00666	Adf00666 Bacterial	C 628	13	81.2	3411	4	ABL08660	Ablo8660 Drosophi1
556	13	81.2	1726	12	ADQ22650	Adq22650 Human sof	C 629	13	81.2	3411	4	ABH62794	Abh62794 Strimp wh
557	13	81.2	1741	6	ABK34581	Abk34581 Human CDN	C 630	13	81.2	3411	8	ABX55221	Abx55221 CDNA enc
558	13	81.2	1759	13	ADRO7047	Adro7047 Full leng	C 631	13	81.2	3411	6	ABE56829	Ab56829 Human mac
559	13	81.2	1776	5	ADL63723	Adl63723 Human ova	C 632	13	81.2	3411	10	ADBS4117	Adbs4117 Human pro
560	13	81.2	1823	12	ADH13780	Adh13780 Human ENZ	C 633	13	81.2	3411	8	ABX34529	Abx34529 Human mdd
561	13	81.2	1849	6	ABL60567	Ablo60567 Human str	C 634	13	81.2	3411	12	AD677047	Ad677047 Human CDN
562	13	81.2	1887	10	ACFE60139	Adfe60139 Human con	C 635	13	81.2	3411	12	AD660217	Ad660217 Concaltene
563	13	81.2	1962	8	ACA52961	Ac52961 Prokaryot	C 636	13	81.2	3411	12	AD045706	Ad045706 Human hll
564	13	81.2	1979	5	ABA15720	Ab15720 Human ner	C 637	13	81.2	3411	12	ADQ64490	Adq64490 Novel imm
565	13	81.2	2052	12	AD080792	Ad080792 Porcine e	C 638	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
566	13	81.2	2119	4	AA158159	AA158159 Human pol	C 639	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
567	13	81.2	2119	5	ADQ98365	Adq98365 DNA encod	C 640	13	81.2	3411	2	AAQ47927	Aaq47927 Ratred ba
568	13	81.2	2119	9	ADB48125	Adb48125 Novel hum	C 641	13	81.2	3411	6	ABN59505	Abn59505 Gene #240
569	13	81.2	2151	12	ADL04227	Adl04227 DNA encod	C 642	13	81.2	3411	10	AD045706	Ad045706 Human hll
570	13	81.2	2163	12	ADH45317	Adh45317 Human enz	C 643	13	81.2	3411	12	ADQ64490	Adq64490 Novel imm
571	13	81.2	2212	6	ABK35505	Abk35505 Human end	C 644	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
572	13	81.2	2286	6	AAL54057	Aal54057 CDNA enc	C 645	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
573	13	81.2	2311	13	ACN40495	Acn40495 Tumour-ab	C 646	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
574	13	81.2	2372	10	ADB62473	Adb62473 Human CDN	C 647	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
575	13	81.2	2440	8	ABX49950	Abx49950 Human CDN	C 648	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
576	13	81.2	2460	12	ADP29128	Adp29128 Human sec	C 649	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
577	13	81.2	2469	10	ADBE1853	Adbe1853 Human CDN	C 650	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
578	13	81.2	2601	8	ACA32877	Ac32877 Prokaryot	C 651	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
579	13	81.2	2604	4	AAS52920	Aas52920 Enterococ	C 652	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
580	13	81.2	2713	8	ACA57245	Ac57245 Human adi	C 653	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
581	13	81.2	2716	13	ADRO7710	Adro7710 Full leng	C 654	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
582	13	81.2	2730	10	ADA52805	Ada52805 Human cod	C 655	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
583	13	81.2	2835	8	ABZ77166	Abz77166 Phoma bec	C 656	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
584	13	81.2	2839	12	ADQ63879	Adq63879 Novel hum	C 657	13	81.2	3411	6	ABK82001	Abk82001 Human DNA
585	13	81.2	2868	2	AAT85578	Aat85578 Murine WS	C 658	13	81.2	3411	13	ADP24242	Adp24242 PRO POLYp
586	13	81.2	2868	9	ACA75468	Ac75468 Mouse DNA	C 659	13	81.2	3411	13	ADP24242	Adp24242 PRO POLYp
587	13	81.2	2868	9	ACH66774	Ach66774 Mouse par	C 660	13	81.2	3411	13	ADP24242	Adp24242 PRO POLYp
588	13	81.2	2868	10	ADCO8099	Adco8099 Partial m	C 661	13	81.2	3411	12	ADP24242	Adp24242 PRO POLYp
589	13	81.2	2923	8	ABT42538	Abt42538 Human nuc	C 662	13	81.2	3411	4	ADP24242	Adp24242 PRO POLYp
590	13	81.2	2931	12	ADQ67246	Adq67246 Novel hum	C 663	13	81.2	3411	10	ADP24242	Adp24242 PRO POLYp
591	13	81.2	2952	12	ADP29129	Adp29129 Human sec	C 664	13	81.2	3411	10	ADP24242	Adp24242 PRO POLYp
592	13	81.2	3114	13	ADR25347	Adr25347 Breast ca	C 665	13	81.2	3411	10	ADP24242	Adp24242 PRO POLYp
593	13	81.2	3132	6	AAS94759	Aas94759 Human DNA	C 666	13	81.2	3411	4	AAK69134	Aak69134 Human imm
594	13	81.2	3132	12	ADQ21319	Adq21319 Human sof	C 667	13	81.2	3411	4	AAK69134	Aak69134 Human imm
595	13	81.2	3140	4	ABL27038	Ab127038 Drosophi1	C 668	13	81.2	3411	6	AAV57416	Aav57416 Tumour su
596	13	81.2	3143	10	ADK41001	Adk41001 Novel hum	C 669	13	81.2	3411	6	AAV57416	Aav57416 Tumour su
597	13	81.2	3143	13	ADRI5715	Adri5715 Klnase 36	C 670	13	81.2	3411	12	ADQ21304	Adq21304 Human sof
598	13	81.2	3206	8	ABX71060	Abx71060 Novel hum	C 671	13	81.2	3411	2	AAV34396	Aav34396 Yellow fe
599	13	81.2	3259	13	ACN39223	Acn39223 Tumour-as	C 672	13	81.2	3411	6	ABA00430	Ab00430 Flaviviru
600	13	81.2	3265	4	ABLO4138	Ablo4138 Drosophi1	C 673	13	81.2	3411	12	ADP24242	Adp24242 PRO POLYp
601	13	81.2	3273	10	ADB47326	Adb47326 Human CDN	C 674	13	81.2	3411	12	ADP24242	Adp24242 PRO POLYp
602	13	81.2	3274	8	ABK62936	Abk62936 Human act	C 675	13	81.2	3411	4	AAK69134	Aak69134 Human imm
603	13	81.2	3411	6	ABK83684	Abk83684 Human CDN	C 676	13	81.2	3411	4	AAK69134	Aak69134 Human imm
604	13	81.2	3411	6	ABN95213	Abn95213 Gene #171	C 677	13	81.2	3411	4	AAK69134	Aak69134 Human imm

678	13	81.2	11839	8	ABZ74494	Secreted	c 751	13	81.2	177531	10	ADB96919	Adb96919 Human MDR
679	13	81.2	11839	8	ADA44503	Human sec	c 752	13	81.2	177531	10	ADB922110	Adb922110 Human MDR
680	13	81.2	12566	8	AAV52282	Streptococ	c 753	13	81.2	177531	10	ADH74617	Adh74617 Human BAC
681	13	81.2	14801	4	AAK79980	Human imm	c 754	13	81.2	209484	11	ACN44126	Acn44126 Human gen
682	13	81.2	14801	4	AAK69135	Human imm	c 755	13	81.2	236233	12	ADQ97590	Adq97590 Human gen
683	13	81.2	14801	4	AAK69915	Human imm	c 756	13	81.2	269223	4	AAK68554	Adk68554 Mouse can
684	13	81.2	14801	4	AAK81361	Human imm	c 757	13	81.2	289137	13	ABD33143	Abd33143 Human gen
685	13	81.2	15500	10	AAK81361	Human imm	c 758	13	81.2	289137	13	ABD33143	Abd33143 Human gen
686	13	81.2	15500	10	ADG41853	Genomic s	c 759	13	81.2	305107	4	AAH62689	Aah62689 Shrimp wh
687	13	81.2	15500	10	ADG41853	Human res	c 759	13	81.2	305107	4	AAH62689	Aah62689 Shrimp wh
688	13	81.2	15576	10	ADP97627	Human res	c 760	13	81.2	313287	13	ABD33100	Abd33100 Human can
689	13	81.2	15773	4	ABE28668	Human GPC	c 761	13	81.2	313287	13	ABD33100	Abd33100 Human can
690	13	81.2	19777	4	AAK89641	Human GPC	c 762	13	81.2	313287	13	ABD33100	Abd33100 Human can
691	13	81.2	22700	4	AAK70746	Human dig	c 763	13	81.2	313287	13	ABD33100	Abd33100 Human can
692	13	81.2	23249	6	AAK70746	Human imm	c 764	13	81.2	313287	13	ABD33100	Abd33100 Human can
693	13	81.2	24187	8	AAK59529	Reference	c 765	13	81.2	313287	13	ABD33100	Abd33100 Human can
694	13	81.2	24187	8	AAK59529	Reference	c 766	13	81.2	313287	13	ABD33100	Abd33100 Human can
695	13	81.2	27204	11	ACN44866	Protonib	c 767	13	81.2	313287	13	ABD33100	Abd33100 Human can
696	13	81.2	27642	4	AAK77486	Human gen	c 768	13	81.2	313287	13	ABD33100	Abd33100 Human can
697	13	81.2	28486	8	AAK77486	Human imm	c 769	13	81.2	313287	13	ABD33100	Abd33100 Human can
698	13	81.2	28486	8	AAK77486	Human imm	c 770	13	81.2	313287	13	ABD33100	Abd33100 Human can
699	13	81.2	28486	8	AAK77486	Human imm	c 771	13	81.2	313287	13	ABD33100	Abd33100 Human can
700	13	81.2	28486	8	AAK77486	Human imm	c 772	13	81.2	313287	13	ABD33100	Abd33100 Human can
701	13	81.2	30781	6	ADP46712	Mouse Ccn	c 773	13	81.2	313287	13	ABD33100	Abd33100 Human can
702	13	81.2	32371	4	ABE111488	Human Ccn	c 774	13	81.2	313287	13	ABD33100	Abd33100 Human can
703	13	81.2	32371	4	ABE111488	Human DBH	c 775	13	81.2	313287	13	ABD33100	Abd33100 Human can
704	13	81.2	33312	10	ADP74372	Human DBH	c 776	13	81.2	313287	13	ABD33100	Abd33100 Human can
705	13	81.2	34739	11	ACN45078	Myobacte	c 777	13	81.2	313287	13	ABD33100	Abd33100 Human can
706	13	81.2	35100	3	AAV20441	Human gen	c 778	13	81.2	313287	13	ABD33100	Abd33100 Human can
707	13	81.2	35133	3	AAK81518	Human gen	c 779	13	81.2	313287	13	ABD33100	Abd33100 Human can
708	13	81.2	35901	2	AAK23892	Human c-f	c 780	13	81.2	313287	13	ABD33100	Abd33100 Human can
709	13	81.2	35902	6	AAK43350	Human c-f	c 781	13	81.2	313287	13	ABD33100	Abd33100 Human can
710	13	81.2	37004	13	ABD33353	Human cyt	c 782	13	81.2	313287	13	ABD33100	Abd33100 Human can
711	13	81.2	37169	13	ABD33258	Human can	c 783	13	81.2	313287	13	ABD33100	Abd33100 Human can
712	13	81.2	38258	6	AAK96633	Human can	c 784	13	81.2	313287	13	ABD33100	Abd33100 Human can
713	13	81.2	38886	2	AAK23897	Murine ca	c 785	13	81.2	313287	13	ABD33100	Abd33100 Human can
714	13	81.2	40152	4	ABE117408	DNA encod	c 786	13	81.2	313287	13	ABD33100	Abd33100 Human can
715	13	81.2	42123	11	ACN44906	Murine LO	c 787	13	81.2	313287	13	ABD33100	Abd33100 Human can
716	13	81.2	44051	13	ADP66992	Human gen	c 788	13	81.2	313287	13	ABD33100	Abd33100 Human can
717	13	81.2	47066	4	ABE11514	Human can	c 789	13	81.2	313287	13	ABD33100	Abd33100 Human can
718	13	81.2	48480	12	ADP47033	Human can	c 790	13	81.2	313287	13	ABD33100	Abd33100 Human can
719	13	81.2	48765	12	ADP61643	Human can	c 791	13	81.2	313287	13	ABD33100	Abd33100 Human can
720	13	81.2	50295	10	ADP02993	Concateme	c 792	13	81.2	313287	13	ABD33100	Abd33100 Human can
721	13	81.2	50295	10	ADP02993	Concateme	c 793	13	81.2	313287	13	ABD33100	Abd33100 Human can
722	13	81.2	50295	10	ADP02993	Concateme	c 794	13	81.2	313287	13	ABD33100	Abd33100 Human can
723	13	81.2	50295	10	ADP02993	Concateme	c 795	13	81.2	313287	13	ABD33100	Abd33100 Human can
724	13	81.2	52211	11	ACN44892	Mouse gen	c 796	13	81.2	313287	13	ABD33100	Abd33100 Human can
725	13	81.2	53714	9	ADA02636	Human DNT	c 797	13	81.2	313287	13	ABD33100	Abd33100 Human can
726	13	81.2	53714	10	ADP72374	Human DNT	c 798	13	81.2	313287	13	ABD33100	Abd33100 Human can
727	13	81.2	57347	13	ABD33274	Human DNT	c 799	13	81.2	313287	13	ABD33100	Abd33100 Human can
728	13	81.2	62130	12	ADP97885	Murine ca	c 800	13	81.2	313287	13	ABD33100	Abd33100 Human can
729	13	81.2	71864	11	ACN45132	Mouse gen	c 801	13	81.2	313287	13	ABD33100	Abd33100 Human can
730	13	81.2	73771	11	ACN45132	Mouse gen	c 802	13	81.2	313287	13	ABD33100	Abd33100 Human can
731	13	81.2	75252	11	ACN44938	Human gen	c 803	13	81.2	313287	13	ABD33100	Abd33100 Human can
732	13	81.2	76146	10	ADL13505	Human gen	c 804	13	81.2	313287	13	ABD33100	Abd33100 Human can
733	13	81.2	80423	13	ABD32576	Osteocarth	c 805	13	81.2	313287	13	ABD33100	Abd33100 Human can
734	13	81.2	80423	13	ABD32576	Osteocarth	c 806	13	81.2	313287	13	ABD33100	Abd33100 Human can
735	13	81.2	87977	9	ADA02639	Mouse can	c 807	13	81.2	313287	13	ABD33100	Abd33100 Human can
736	13	81.2	87977	10	ADP72377	Mouse can	c 808	13	81.2	313287	13	ABD33100	Abd33100 Human can
737	13	81.2	87977	10	ADP72377	Mouse can	c 809	13	81.2	313287	13	ABD33100	Abd33100 Human can
738	13	81.2	92638	6	ABQ88096	Mouse Znf	c 810	13	81.2	313287	13	ABD33100	Abd33100 Human can
739	13	81.2	106416	4	ABE18718	Human ost	c 811	13	81.2	313287	13	ABD33100	Abd33100 Human can
740	13	81.2	107036	13	ABD33557	Drosophill	c 812	13	81.2	313287	13	ABD33100	Abd33100 Human can
741	13	81.2	110000	3	AAH81489	Continuation (4 of	c 813	13	81.2	313287	13	ABD33100	Abd33100 Human can
742	13	81.2	110000	3	AAH81489	Continuation (18 of	c 814	13	81.2	313287	13	ABD33100	Abd33100 Human can
743	13	81.2	110000	11	ACN43398	Continuation (2 of	c 815	13	81.2	313287	13	ABD33100	Abd33100 Human can
744	13	81.2	110000	13	ABD32968	Continuation (4 of	c 816	13	81.2	313287	13	ABD33100	Abd33100 Human can
745	13	81.2	110000	13	ABD32968	Continuation (5 of	c 817	13	81.2	313287	13	ABD33100	Abd33100 Human can
746	13	81.2	125466	13	ABD32780	Continuation (5 of	c 818	13	81.2	313287	13	ABD33100	Abd33100 Human can
747	13	81.2	147708	6	ABD32897	Human can	c 819	13	81.2	313287	13	ABD33100	Abd33100 Human can
748	13	81.2	147708	6	ABD32897	Human can	c 820	13	81.2	313287	13	ABD33100	Abd33100 Human can
749	13	81.2	177531	8	ACF62732	Human ost	c 821	13	81.2	313287	13	ABD33100	Abd33100 Human can
750	13	81.2	177531	8	ACF62732	Cancer ba	c 822	13	81.2	313287	13	ABD33100	Abd33100 Human can
	13	81.2	177531	10	ADB87936	MRP1 base	c 823	13	81.2	313287	13	ABD33100	Abd33100 Human can
	13	81.2	177531	10	ADB87936	Human UGT	c 823	13	81.2	313287	13	ABD33100	Abd33100 Human can

824	12	75.0	32	6	AAD25631	Ad25631 Oligo #11	C 897	12	75.0	386	4	AAK01591	Aak01591 Human bra
825	12	75.0	32	6	AAD25629	Ad25629 Oligo #9,	C 898	12	75.0	386	4	ABS26620	Abs26620 Human liv
826	12	75.0	32	6	AAD25627	Ad25627 Oligo #7,	C 899	12	75.0	386	5	AAI01561	Aai01561 Probe #15
827	12	75.0	41	2	AAV65931	Aav65931 Oligonuclei	C 900	12	75.0	387	5	AAFG5293	Aafg5293 Novel hum
828	12	75.0	41	7	ADI93044	Adi93044 Hepatic tis	C 901	12	75.0	382	4	AAI13376	Aai13376 Probe #33
829	12	75.0	43	6	ADBS3001	Adbs3001 FEN-1 rel	C 902	12	75.0	382	4	ABAS5073	Abas5073 Human foe
C 830	12	75.0	53	12	ADN36217	Adn36217 Probe #29	C 903	12	75.0	382	4	AAI34730	Aai34730 Probe #34
C 831	12	75.0	53	12	ADN36055	Aax34322 Human bet	C 904	12	75.0	382	4	ABAA4622	Abaa4622 Human bre
C 832	12	75.0	64	2	AAX34322	Aax34322 Human bet	C 905	12	75.0	382	4	ABA24826	Aba24826 Probe #32
C 833	12	75.0	65	6	ABN33049	Abn33049 Rat splic	C 906	12	75.0	382	4	AAK28789	Aak28789 Human bon
C 834	12	75.0	65	6	ABN30919	Abn30919 Rat splic	C 907	12	75.0	382	4	AAK03338	Aak03338 Human bra
C 835	12	75.0	100	8	ACD78395	Acad78395 E. coli K	C 908	12	75.0	382	4	ABSS28393	Abss28393 Human liv
C 836	12	75.0	126	3	AAAC18203	Aac18203 Human sec	C 909	12	75.0	382	5	AAI03270	Aai03270 Probe #32
C 837	12	75.0	141	6	ABN60348	Abn60348 Human can	C 910	12	75.0	382	6	ABSO3316	Abso3316 Human gen
C 838	12	75.0	144	10	ADF73102	Adf73102 Nucleotid	C 911	12	75.0	392	6	ACLI33223	Accli33223 DNA clone
C 839	12	75.0	149	12	AD013517	Ad013517 SNP target	C 912	12	75.0	395	12	AD016406	Ad016406 Nucleotid
C 840	12	75.0	158	9	ACLI3377	Accli3377 DNA clone	C 913	12	75.0	396	4	AAFP94868	Aafp94868 Human ova
C 841	12	75.0	177	2	AAQ72531	Aaq72531 Osteoclas	C 914	12	75.0	386	6	ABL48818	Abli48818 Ovarian c
C 842	12	75.0	177	6	ABN86720	Abn86720 Human ovt	C 915	12	75.0	386	6	ABT03135	Abt03135 Human ova
C 843	12	75.0	185	6	AAD37113	Ad37113 Human pho	C 916	12	75.0	386	11	ADM10728	Adm10728 Human ova
C 844	12	75.0	189	7	ADS69752	Ads69752 Corn seed	C 917	12	75.0	396	12	ADJ11058	Adj11058 Represent
C 845	12	75.0	219	4	AAI27063	Aai27063 Probe #16	C 918	12	75.0	396	12	ADM43319	Adm43319 Human ova
C 846	12	75.0	219	4	ABA75333	Abat75333 Human foe	C 919	12	75.0	387	8	ABX37270	Abx37270 Bovine ES
C 847	12	75.0	219	4	AAI55899	Aai55899 Probe #24	C 920	12	75.0	388	4	AAI23887	Aai23887 Probe #13
C 848	12	75.0	219	4	ABA33978	Abat33978 Probe #18	C 921	12	75.0	388	4	AAI14693	Aai14693 Probe #46
C 849	12	75.0	219	4	AAK49692	Aak49692 Human bon	C 922	12	75.0	388	4	ABA69006	Abat69006 Human foe
C 850	12	75.0	219	4	AAK23888	Aak23888 Human bra	C 923	12	75.0	388	4	ABAS64425	Abas64425 Human foe
C 851	12	75.0	219	4	ABSA49609	Abat49609 Human liv	C 924	12	75.0	388	4	AAI49195	Aai49195 Probe #17
C 852	12	75.0	219	4	ABSS23452	Abat23452 Human gen	C 925	12	75.0	388	4	AAI36060	Aai36060 Probe #47
C 853	12	75.0	223	8	ABX52786	Abx52786 Bovine ES	C 926	12	75.0	388	4	ABAA45898	Abat45898 Human bra
C 854	12	75.0	226	2	AAK39488	Aax39488 Human sec	C 927	12	75.0	388	4	ABAA51016	Abat51016 Human bra
C 855	12	75.0	240	6	ABL83299	Abli83299 Human ova	C 928	12	75.0	388	4	ABAA5950	Abat5950 Probe #14
C 856	12	75.0	242	6	ABN17691	Abn17691 Human ORF	C 929	12	75.0	388	4	ABAA26057	Abat26057 Probe #45
C 857	12	75.0	243	12	ADL03735	Adl03735 DNA, enco	C 930	12	75.0	388	4	AAK30097	Aak30097 Human bon
C 858	12	75.0	253	6	ABL78183	Abli78183 Human ova	C 931	12	75.0	388	4	AAK43118	Aak43118 Human bon
C 859	12	75.0	257	6	ABL87535	Abli87535 Human ova	C 932	12	75.0	388	4	AAK04590	Aak04590 Human bra
C 860	12	75.0	257	6	ABL84726	Abli84726 Human ova	C 933	12	75.0	388	4	AAK17325	Aak17325 Human bra
C 861	12	75.0	258	11	ADL98233	Adl98233 Human tum	C 934	12	75.0	388	4	ABSA42752	Abat42752 Human liv
C 862	12	75.0	279	9	ACLI3313	Accli3313 DNA clone	C 935	12	75.0	388	4	ABSA29747	Abat29747 Human liv
C 863	12	75.0	284	6	ABL72537	Abli72537 Corn tass	C 936	12	75.0	388	5	AAI04499	Aai04499 Probe #44
C 864	12	75.0	287	10	ABX84480	Abx84480 Corn ear-	C 937	12	75.0	388	5	AAI09489	Aai09489 Probe #94
C 865	12	75.0	290	6	ABL73350	Abli73350 Corn tass	C 938	12	75.0	388	6	ABSI17192	Abat17192 Human gen
C 866	12	75.0	290	6	ACLI3357	Accli3357 DNA clone	C 939	12	75.0	388	6	ABSO4676	Abat4676 Human gen
C 867	12	75.0	308	6	ABL87220	Abli87220 Human ova	C 940	12	75.0	403	4	AAI91430	Aai91430 Human pol
C 868	12	75.0	310	4	AAK83938	Aak83938 Human imm	C 941	12	75.0	404	8	ABZ56406	Abz56406 Aspergill
C 869	12	75.0	313	6	ABO98681	Abog98681 Human ORF	C 942	12	75.0	404	9	ACLI3341	Accli3341 DNA clone
C 870	12	75.0	319	10	ADF85706	Adf85706 Human ade	C 943	12	75.0	405	13	ACN61537	Acn61537 Cotton gy
C 871	12	75.0	320	6	ABL66069	Abli66069 Lung canc	C 944	12	75.0	407	2	AAZ34254	Aaz34254 Human EST
C 872	12	75.0	322	9	ACLI3369	Accli3369 DNA clone	C 945	12	75.0	407	3	AACT8564	Aact8564 Human EST
C 873	12	75.0	323	4	AAI98608	Aai98608 Human exc	C 946	12	75.0	407	8	ACA63822	Aca63822 Novel hum
C 874	12	75.0	323	5	AAI63004	Aai63004 Human kid	C 947	12	75.0	407	8	ACA71986	Aca71986 Human PRO
C 875	12	75.0	326	9	ACLI3335	Accli3335 DNA clone	C 948	12	75.0	407	8	ABX92626	Abx92626 Human PRO
C 876	12	75.0	328	6	ABV94088	Abv94088 Breast ca	C 949	12	75.0	407	8	ACA63637	Acad63637 Human sec
C 877	12	75.0	332	9	ACLI3316	Accli3316 DNA clone	C 950	12	75.0	407	9	ADA24970	Ada24970 Novel hum
C 878	12	75.0	334	3	ACLI3254	Accli3254 DNA clone	C 951	12	75.0	407	9	ACD29968	Acad29968 Novel hum
C 879	12	75.0	344	3	AAC06746	Aac06746 Human sec	C 952	12	75.0	407	9	ADAI12631	Adai12631 Human sec
C 880	12	75.0	346	5	ABAI3740	Abai3740 Human ner	C 953	12	75.0	407	9	ACD29383	Acad29383 Novel hum
C 881	12	75.0	351	4	ABA06677	Abat06677 Human CDN	C 954	12	75.0	407	9	ACLI33331	Accli33331 DNA clone
C 882	12	75.0	351	6	ABV84014	Abv84014 Human pol	C 955	12	75.0	407	10	ADB73937	Adb73937 Human PRO
C 883	12	75.0	354	2	AAV04511	Aav04511 Osteoclas	C 956	12	75.0	407	10	ADB76653	Adb76653 Human PRO
C 884	12	75.0	361	9	ACLI3372	Accli3372 DNA clone	C 957	12	75.0	407	10	ADC44079	Adc44079 Human EST
C 885	12	75.0	364	10	ADD27665	Add27665 Human adt	C 958	12	75.0	407	10	ADC61839	Adc61839 Human EST
C 886	12	75.0	367	9	ACLI3330	Accli3330 DNA clone	C 959	12	75.0	407	10	ADC63803	Adc63803 Human EST
C 887	12	75.0	373	2	ACLI3270	Accli3270 DNA clone	C 960	12	75.0	407	10	ADC66903	Adc66903 Human EST
C 888	12	75.0	376	2	AAK33548	Aak33548 Human sec	C 961	12	75.0	407	10	ADC69027	Adc69027 Human EST
C 889	12	75.0	376	10	ADK56201	Adk56201 Plant DNA	C 962	12	75.0	407	10	ADC63087	Adc63087 Human EST
C 890	12	75.0	378	5	ABV18153	Abv18153 Human pro	C 963	12	75.0	407	10	ADC68152	Adc68152 Human EST
C 891	12	75.0	385	6	ABK45359	Abk45359 CDNA enco	C 964	12	75.0	407	10	ADC41472	Adc41472 Human EST
C 892	12	75.0	386	4	AAI11634	Aai11634 Probe #15	C 965	12	75.0	407	10	ADC67527	Adc67527 Human EST
C 893	12	75.0	386	4	ABAS3326	Abas3326 Human foe	C 966	12	75.0	407	10	ADC62463	Adc62463 Human EST
C 894	12	75.0	386	4	ABAA2905	Abaa2905 Human bre	C 967	12	75.0	407	10	ADC42096	Adc42096 Human EST
C 895	12	75.0	386	4	ABAZ103	Abaz103 Probe #15	C 968	12	75.0	407	10	ADBA49465	Adba49465 Human EST
C 896	12	75.0	386	4	AAK27034	Aak27034 Human bon	C 969	12	75.0	407	10	ADBS35519	Adbs35519 Human EST

C 970	12	75.0	407	10	ADe16633	Human EST
C 971	12	75.0	407	10	ADd73248	Human EST
C 972	12	75.0	407	10	ADd72606	Human EST
C 973	12	75.0	407	10	ADe17257	Human EST
C 974	12	75.0	407	10	ADP47271	Human EST
C 975	12	75.0	407	10	ADG53028	Human EST
C 976	12	75.0	407	10	ADG60348	Human EST
C 977	12	75.0	407	10	ADG61108	Human EST
C 978	12	75.0	407	10	ADd42787	Novel hum
C 979	12	75.0	407	10	ADd48765	Human EST
C 980	12	75.0	407	12	ADd89866	Human EST
C 981	12	75.0	407	12	ADd61506	Human EST
C 982	12	75.0	407	12	ADd40198	Human EST
C 983	12	75.0	407	12	ADd45994	Human EST
C 984	12	75.0	407	12	ADd24390	Human EST
C 985	12	75.0	407	12	ADd40822	Human EST
C 986	12	75.0	407	12	ADd23766	Human EST
C 987	12	75.0	407	12	ADd33749	Human EST
C 988	12	75.0	407	12	ADd27216	Human EST
C 989	12	75.0	407	12	ADd27852	Human EST
C 990	12	75.0	407	12	ADd41446	Human EST
C 991	12	75.0	407	12	ADdF3125	Human EST
C 992	12	75.0	407	12	ADdF25491	Human EST
C 993	12	75.0	407	12	ADdF2592	Human EST
C 994	12	75.0	407	12	ADdF34381	Human EST
C 995	12	75.0	407	12	ADdF46618	Human EST
C 996	12	75.0	407	12	ADdG50604	Human EST
C 997	12	75.0	407	12	ADdG49980	Human EST
C 998	12	75.0	407	12	ADdG51852	Human EST
C 999	12	75.0	407	12	ADdG49356	Human EST
C1000	12	75.0	407	12	ADdG48732	Human EST

ALIGNMENTS

RESULT 1

AA18256
ID AA18256 standard; DNA, 16 BP.

AC AA18256;

DT 17-SEP-1996 (first entry)

DE HBV epsilon encapsidation mRNA intermediate antisense oligo 12c.

XX Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
XX epsilon; encapsidation; sequence; intermediate; subtype ayw; C gene;
KW treatment; chronic infection; modulation; translation; transcription;
KM release; host cell; ss.

XX Synthetic.

XX PN WO9603152-A1.

XX PD 08-FEB-1996.

XX PF 28-JUL-1995; 95WO-US009143.

XX PR 28-JUL-1994; 94US-00281106.

XX PA (GEO) UNIV GEORGETOWN.

XX PI Korba BE, Gerin JL;

XX DR WPI, 1996-116796/12.

XX Single stranded oligo:nucleotide(s) for inhibiting replication of
PT hepatitis B virus - are anti-sense to portions of the epsilon
XX encapsidation sequence and modulate HBV function.

PS Claim 15; Page 44; 56pp; English.

CC The present sequence, which inhibits the replication of hepatitis B virus
CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that
CC binds the epsilon encapsidation sequence of a mRNA intermediate derived
CC from the HBV genome. The 1st nucleotide of the oligonucleotide
CC corresponds to nucleotide 1894 of the HBV ayw subtype C gene, using the
CC numbering scheme from the sequence published by Galibert et al., Nature
CC 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to
CC treat chronic HBV infection by modulating a HBV related function, e.g.
CC translation, transcription, encapsidation, replication and release from a
CC host cell. The effect of the oligonucleotide on the levels of HBV DNA in
CC the extracellular medium (VIR. DNA), intracellular viral replicative
CC intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface
CC antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core
CC treatment) or ND (not determined), given as the EC(90) (microm, 9 days of
CC RNA (>20), HBsAg (>20), HBeAg (>20) and HBeAg (18.5)

SQ Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 16; DB 2; Length 16;
Best local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGCA 16
Db 1 AAAGCCACCCCAAGCA 16

RESULT 2

AAV14125
ID AAV14125 standard; DNA, 16 BP.

XX AC AAV14125;

DT 27-ANG-2003 (revised)

DT 19-MAY-1998 (first entry)

DE Probe HBP141 for preCore region of HBV.

XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KM mutation detection; ss.

XX OS Synthetic.

XX OS Hepatitis B virus.

XX PN WO9740193-A2.

XX PD 30-OCT-1997.

XX PF 21-APR-1997; 97WO-EP002002.

XX PR 19-APR-1996; 96EP-00870053.

XX PA (INNO-) INNOGENETICS NV.

XX PI Stuyver L, Rossau R, Maertens G;

XX DR WPI, 1997-535867/49.

XX Detection and/or genetic analysis of hepatitis B virus - specifically
PT genotype, preCore mutations, vaccine escape mutations and RT gene
PT mutations selected by treatment with drugs.

XX Claim 5; Page 27; 80pp; English.

XX This sequence represents a probe for the preCore region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleotide acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridizing (I) with a combination of at least

CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected for treatment with drugs, e.g. lamivudine and
 CC penciclovir. (updated on 27-AUG-2003 to correct OS field.)

XX Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16

RESULT 3

ID ADB68575 standard; DNA; 16 BP.

XX ADB68575;

AC 04-DEC-2003 (first entry)

DE NG3 A-L-P conjugate DNA component used to target HBV e-site.

XX homogeneous A-L-P conjugate; hepatic; chronic viral hepatitis; cirrhosis;
 KM malaria; viral infection; protozoan; cancer; hepatocellular carcinoma;
 KM HCC; ss; NG3; HBV; e-site; pregenome.

XX Hepatitis B virus.

FM Key Location/Qualifiers

FT modified_base 1..16

FT /*tag= b /mod_base= OTHER

FT /note= "OTHER = phosphorothioate backbone"

FT modified_base 1

FT /*tag= a /mod_base= OTHER

FT /note= "OTHER = Optionally linked to YEE(a)ga1Nac)3-SMCC

FT and various chemical groups as shown in figures"

FT modified_base 16

FT /*tag= c /mod_base= OTHER

FT /note= "OTHER = Optionally linked to chemical group as

FT shown in figure 5"

FM WO2003067209-A2.

XX 14-AUG-2003.

XX 21-JUN-2002; 2002WO-US019908.

XX 22-JUN-2001; 2001US-00888164.

XX (CELL-) CELL WORKS INC.

XX (UYJO) UNIT JOHNS HOPKINS.

XX Te'o POP, Duff R, Zhou Y, Deamond S, Roby C;

XX WPI; 2003-697456/66.

XX New homogeneous prodrgng conjugate containing hepatic ligand for delivery
 PT of pathogen-specific oligomer useful for treating liver infections or
 PT cancer.

XX Claim 7; Page 83; 107bp; English.

XX The invention relates to a novel homogeneous conjugate comprising a
 CC hepatic ligand, bifunctional linker and biologically stable oligomer that
 CC binds to a sequence in a hepatic virus or pathogen and is released from
 CC the conjugate by hydrolysis or reduction. The conjugate of the invention
 CC may be useful during the treatment of liver diseases including chronic
 CC viral hepatitis, cirrhosis, malaria, viral or protozoan infection and
 CC cancer, such as hepatocellular carcinoma (HCC). The current sequence is
 CC that of the NG3 A-L-P conjugate DNA component of the invention which was
 CC used to target the Hepatitis B virus (HBV) pregenome (e-site).

XX Sequence 16 BP; 7 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16

RESULT 4

ID ACD55710 standard; RNA; 17 BP.

XX ACD55710;

AC 23-SEP-2003 (first entry)

DE HBV amberyzyme substrate sequence #183.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KM RNA stability; RNA expression; RNA synthesis; antisense;
 KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
 KM amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KM HBV reverse transcriptase; Enhancer I region; viral replication;
 KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KM virucide; antiinflammatory; substrate; ss.

FM Hepatitis B virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT) BLATT L.

XX (MACE) MACEJAK D.

XX (MCSW) MCSWIGEN J.

XX (MORR) MORRISSEY D.

XX (PAVC) PAVCO P.

XX (LEEP) LEE P.

XX (DRAP) DRAPER K.

XX (ROBE) ROBERTS E.

XX Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus infection.

PS Example 1; Page 207; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zincymes, ambezymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents a substrate for one of the HBV

CC ribozyme, inozyme, G-cleaver, zincyme, DNazyme or ambezyme sequences

CC disclosed in the present invention

CC

SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGGCA 16

DB 17 AAAGCCACCCCAAGGCA 2

RESULT 5

ID ACD53930 standard; RNA; 17 BP.

XX ACD53930;

AC ACD53930;

XX

DT 24-SEP-2003 (first entry)

XX

DE HBV zincyme substrate sequence #100.

XX

KM Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

KM RNA stability; RNA expression; RNA synthesis; antisense;

KM enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zincyme;

KM ambezyme; G-cleaver ribozyme; decoy molecule; aptamer;

KM HBV reverse transcriptase; Enhancer I region; viral replication;

KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;

KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

KM virucide; antiinflammatory; substrate; ss.

XX

OS Hepatitis B virus.

XX

PN WO200281494-A1.

XX

PD 17-OCT-2002.

XX

PF 26-MAR-2002; 2002WO-US009187.

XX

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVCO/) PAVCO P.

PA (LEE/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX

PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P,

PI Draper K, Roberts E;

XX

DR WPI; 2003-229207/22.

XX

PT Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX

PS Example 1; Page 175; 387pp; English.

XX

CC The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zincymes, ambezymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents a substrate for one of the HBV

CC ribozyme, inozyme, G-cleaver, zincyme, DNazyme or ambezyme sequences

CC disclosed in the present invention

CC

SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGGCA 16

DB 16 AAAGCCACCCCAAGGCA 1

RESULT 6

ID ADM59621 standard; RNA; 17 BP.

XX ADM59621;

AC ADM59621;

XX

DT 03-JUN-2004 (first entry)

XX

DE Hepatitis B virus (HBV) RNA target sequence #1755.

XX

KM Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;

KM hepatitis B virus infection; hepatitis; hepatocellular carcinoma;

KM cirrhosis; liver failure; lamivudine; interferon; genetic drift;

KM virucide; hepatotropic; antiinflammatory; cytostatic.

XX

OS Hepatitis B virus.

XX

PN US2004054156-A1.

XX

PD 18-MAR-2004.

XX

PF 15-JAN-2003; 2003US-00342902.

XX

XX 14-MAY-1992; 92US-00882712.

PR 07-FEB-1994; 94US-00193627.

PR 08-NOV-1999; 99US-00436430.

PR 20-MAR-2000; 2000US-00531025.

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PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP/) DRAPER K.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (MORR/) MORRISSEY D.
XX
XX Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
XX specifically cleaving RNA derived from hepatitis B virus and comprising
XX one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 1755; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
XX specifically cleaves RNA derived from hepatitis B virus (HBV) and
XX comprising one or more binding arms, without requiring the presence of a
XX 2'-OH group within the molecule for activity. The nucleic acids are
XX useful for treating hepatitis B virus infection, hepatitis,
XX hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
XX combination with other therapies such as lamivudine and interferons. The
XX nucleic acids are useful as diagnostic tools to examine genetic drift and
XX mutations within diseased cells, for detecting the presence of HBV RNA in
XX a cell, for the study of RNA and for down-regulating gene expression of
XX target genes in bacterial, fungal, viral, plant or mammalian cells. This
XX sequence represents an HBV RNA target sequence, used in the scope of the
XX invention. Note: The sequence data for this patent is also available in
XX electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 16; DB 12; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 9.5;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGCCACCCCAAGGCA 16
DB 16 AAGGCCACCCCAAGGCA 1
XX
RESULT 7
ADM60244/c
ID ADM60244 standard; RNA; 17 BP.
XX
XX ADM60244;
XX
XX 03-JUN-2004 (first entry)
XX
XX Hepatitis B virus (HBV) RNA target sequence #2378.
XX
XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
XX hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
XX cirrhosis; liver failure; lamivudine; interferon; genetic drift;
XX virulence; hepatotropic; antiinflammatory; cytosstatic.
XX
XX Hepatitis B virus.
XX
XX US2004054156-A1.
XX
XX 18-MAR-2004.
XX
XX 15-JAN-2003; 2003US-00342902.
XX
XX 14-MAY-1992; 92US-00882712.
XX 07-FEB-1994; 94US-00193627.
XX 08-NOV-1999; 99US-00436430.
XX 20-MAR-2000; 2000US-00531025.
XX 09-AUG-2000; 2000US-00636385.
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PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP/) DRAPER K.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (MORR/) MORRISSEY D.
XX
XX Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
XX specifically cleaving RNA derived from hepatitis B virus and comprising
XX one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 2378; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
XX specifically cleaves RNA derived from hepatitis B virus (HBV) and
XX comprising one or more binding arms, without requiring the presence of a
XX 2'-OH group within the molecule for activity. The nucleic acids are
XX useful for treating hepatitis B virus infection, hepatitis,
XX hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
XX combination with other therapies such as lamivudine and interferons. The
XX nucleic acids are useful as diagnostic tools to examine genetic drift and
XX mutations within diseased cells, for detecting the presence of HBV RNA in
XX a cell, for the study of RNA and for down-regulating gene expression of
XX target genes in bacterial, fungal, viral, plant or mammalian cells. This
XX sequence represents an HBV RNA target sequence, used in the scope of the
XX invention. Note: The sequence data for this patent is also available in
XX electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 16; DB 12; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 9.5;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGCCACCCCAAGGCA 16
DB 17 AAGGCCACCCCAAGGCA 2
XX
RESULT 8
AAT71786
ID AAT71786 standard; DNA; 18 BP.
XX
XX AAT71786;
XX
XX 29-AUG-1997 (first entry)
XX
XX Hepatitis B virus precore antigen wild-type target sequence primer.
XX
XX HBV; ligase chain reaction; internal standard; amplification; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_difference 1
XX FT /*tag= a
XX FT /note= "Phosphorylated"
XX FT misc_difference 18
XX FT /*tag= b
XX FT /note= "Haptenated with fluorescein"
XX
XX MO9640996-A1.
XX
XX 19-DEC-1996.
XX
XX 03-JUN-1996; 96WO-US008429.
XX 07-JUN-1995; 95US-00480220.
```



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XX (ABBO ) ABBOTT LAB.
XX Birkenmeyer L, Mushahwar IK;
XX WPI, 1997-052367/05.
XX Quantitative detection of target nucleic acid sequence, esp. hepatitis B
XX virus - can distinguish wild-type and mutant DNA types.
XX Claim 14; Page 29; 40pp; English.
XX A novel method has been produced for detecting the amount of a target
XX nucleic acid sequence which may be present in a test sample. It involves
XX contacting the test sample with means for performing a nucleic acid
XX amplification reaction; and determining the ratio of target amplification
XX products to internal standard amplification products present in the
XX sample. The present sequence represents a primer/target specific probe
XX for the hepatitis B virus (HBV) preCore antigen wild-type target sequence
XX (AAV71783). The method can be used for distinguishing between two
XX different nucleic acid sequences present in a sample e.g. wild-type and
XX mutant. The compositions can be used for quantitatively detecting the DNA
XX of HBV.
XX Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 16; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.5;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAAGCCACCCAGGCA 16
XX 1 AAAGCCACCCAGGCA 16
XX
XX RESULT 9
XX ID AAV14133 standard; DNA; 18 BP.
XX AC AAV14133;
XX AC 27-AUG-2003 (revised)
XX DT 19-MAY-1998 (first entry)
XX XX
XX DE Probe HBPr49 for preCore region of HBV.
XX XX
XX KW Probe; hepatitis B virus; HBV detection; RT pol region; genetic analysis;
XX KW preCore region; HBsAg region; genotype specific target;
XX KW mutation detection; ss.
XX XX
XX OS Synthetic.
XX OS Hepatitis B virus.
XX XX
XX PN WO9740193-A2.
XX PD 30-OCT-1997.
XX PD 21-APR-1997; 97WO-EP002002.
XX PF 19-APR-1996; 96EP-00870053.
XX PR
XX XX (INNO-) INNOGENETICS NV.
XX PA
XX PI Stuyver L, Rossau R, Maertens G,
XX PT WPI, 1997-535867/49.
XX PT Detection and/or genetic analysis of hepatitis B virus - specifically
XX PT genotype, preCore mutations, vaccine escape mutations and RT gene
XX PT mutations selected by treatment with drugs.
XX PS Claim 5; Page 27; 80pp; English.
XX

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CC This sequence represents a probe for the preCore region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (1) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (1) with a combination of at least
CC 2 nucleotide probes, which are applied to known locations on a solid
CC support and hybridise specifically to mutant target sequences chosen from
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and interfering
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 18 BP; 8 A; 7 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 16; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.5;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAAGCCACCCAGGCA 16
XX 1 AAAGCCACCCAGGCA 16
XX
XX RESULT 10
XX ID AAT71785/c
XX AC AAT71785;
XX AC 29-AUG-1997 (first entry)
XX DT
XX DE Hepatitis B virus preCore antigen wild-type target sequence primer.
XX DE HBV; ligase chain reaction; internal standard; amplification; ss.
XX XX
XX OS Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX FT misc_difference 1 /*tag= a
XX FT /note= "Haptenated with fluoroscein"
XX FT
XX XX
XX PN WO9640996-A1.
XX PD 19-DEC-1996.
XX PD 03-JUN-1996; 96WO-US008429.
XX PF 07-JUN-1995; 95US-00480220.
XX PR
XX XX (ABBO ) ABBOTT LAB.
XX PA
XX PI Birkenmeyer L, Mushahwar IK;
XX PT WPI, 1997-052367/05.
XX PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
XX PT virus - can distinguish wild-type and mutant DNA types.
XX PT Claim 14; Page 29; 40pp; English.
XX A novel method has been produced for detecting the amount of a target
XX nucleic acid sequence which may be present in a test sample. It involves
XX contacting the test sample with means for performing a nucleic acid
XX amplification reaction; and determining the ratio of target amplification
XX products to internal standard amplification products present in the
XX

```

CC sample. The present sequence represents a primer/target specific probe
CC for the hepatitis B virus (HBV) precore antigen wild-type target sequence
CC (AAAT1783). The method can be used for distinguishing between two
CC different nucleic acid sequences present in a sample e.g. wild-type and
CC mutant. The compositions can be used for quantitatively detecting the DNA
CC of HBV
XX
SQ Sequence 19 BP; 0 A; 3 C; 8 G; 8 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 16; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3
DB
RESULT 11
AAAT1789/c
ID AAAT1789 standard; DNA; 19 BP.
XX
AC AAAT1789;
XX
DT 29-AUG-1997 (first entry)
XX
DE Hepatitis B virus precore antigen mutant target sequence primer.
XX
KW HBV, ligase chain reaction; internal standard; amplification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1/*tag= a
FT /note= "Haptenated with fluorescein"
XX
PN WC9640996-A1.
XX
PD 19-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008429.
XX
PR 07-JUN-1995; 95US-00480220.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Birkemeyer L, Mushahwar IK;
XX
DR WPI; 1997-052367/05.
XX
PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT virus - can distinguish wild-type and mutant DNA types.
XX
PS Claim 14; Page 30; 40pp; English.
XX
CC A novel method has been produced for detecting the amount of a target
CC nucleic acid sequence which may be present in a test sample. It involves
CC contacting the test sample with means for performing a nucleic acid
CC amplification reaction, and determining the ratio of target amplification
CC products to internal standard amplification products present in the
CC sample. The present sequence represents a primer/target specific probe
CC for the hepatitis B virus (HBV) precore antigen mutant target sequence
CC (AAAT1784). The method can be used for distinguishing between two
CC different nucleic acid sequences present in a sample e.g. wild-type and
CC mutant. The compositions can be used for quantitatively detecting the DNA
CC of HBV
XX
SQ Sequence 19 BP; 1 A; 3 C; 7 G; 8 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 16; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3
DB
RESULT 12
ADM00160/c
ID ADM00160 standard; RNA; 19 BP.
XX
AC ADM00160;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hepatitis B virus short interfering nucleic acid (siNA) #576.
XX
KW Viruslike; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KW siNA; hepatitis B virus; HBV; RNA interference.
XX
OS Hepatitis B virus.
XX
PN US2003206687-A1.
XX
PD 06-NOV-2003.
XX
PF 16-SEP-2002; 2002US-00244647.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436330.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
XX
XX (MORR/) MORRISSEY D.
PA (MCSW/) MCSWIGEN J A.
PA (BEIG/) BEIGELMAN L.
XX
PI Morrissey D, Mcswigen JA, Beigelman L;
XX
DR WPI; 2003-901032/82.
XX
PT New short interfering nucleic acid molecules which down-regulates
PT expression of a hepatitis B virus (HBV) or which inhibits HBV
PT replication, useful for treating human HBV infections or for
PT characterizing gene function.
XX
PS Claim 11; Page 48; 72pp; English.
XX
CC The invention relates to a short interfering nucleic acid (siNA) molecule
CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
CC interference or that inhibits HBV replication. Also disclosed are the
CC following: (i) a method of modulating the expression of a HBV gene in a
CC tissue explant; (ii) a method of generating a library of siNA constructs
CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv) a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC and an antisense region, where the antisense region comprises sequence
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA

CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprises separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterising pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.

SO Sequence 19 BP; 0 A; 3 C; 9 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCAAGCA 16
 DB 16 AAAGCCACCAAGCA 1

RESULT 13
 ADM00806
 ID ADM00806 standard; RNA; 19 BP.

AC ADM00806;
 DT 20-MAY-2004 (first entry)
 XX
 DE Hepatitis B virus short interfering nucleic acid (siNA) #1222.

XX
 KM Vincide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KW siNA; hepatitis B virus; HBV; RNA interference.

XX Hepatitis B virus.

XX US2003206887-A1.

XX 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.

XX (MORR/) MORRISSEY D.
 PA (MCSM/) MCSMIGEN J A.
 PA (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswigen JA, Beigelman L;

DR WPI; 2003-901032/82.

XX New short interfering nucleic acid molecules which down-regulate
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.

XX Claim 11; Page 48; 72pp; English.

XX The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesising a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises a sense
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprises separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterising pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.

SO Sequence 19 BP; 7 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCAAGCA 16
 DB 4 AAAGCCACCAAGCA 19

RESULT 14
 ADM00807
 ID ADM00807 standard; RNA; 19 BP.

AC ADM00807;
 DT 20-MAY-2004 (first entry)
 XX
 DE Hepatitis B virus short interfering nucleic acid (siNA) #1223.

XX
 KM Vincide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KW siNA; hepatitis B virus; HBV; RNA interference.

XX Hepatitis B virus.

XX US2003206887-A1.

XX 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.

PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US009287.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSM/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 48; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 19 BP; 8 A; 8 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCACCACCAAGCA 16
 |||||
 Db 2 AAAGCACCACCAAGCA 17
 |||||
 RESULT 15

ADM00284
 ID ADM00284 standard; RNA; 19 BP.
 XX
 AC ADM00284;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Hepatitis B virus short interfering nucleic acid (siNA) #700.
 XX
 KW Virusidae; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KW siNA; hepatitis B virus; HBV; RNA interference.
 OS Hepatitis B virus.
 XX
 PN US2003206887-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 16-SEP-2002; 2002US-00244647.
 XX
 PR 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSM/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 41; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal

CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 CC
 SQ Sequence 19 BP; 8 A; 7 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAAAGCA 16
 DB 1 AAAGCCACCCAAAGCA 16

RESULT 16
 ADM00804
 ID ADM00804 standard; RNA; 19 BP.

AC ADM00804;
 DT 20-MAY-2004 (first entry)

DE Hepatitis B virus short interfering nucleic acid (siNA) #1220.

KW siNA; hepatitis B virus; HBV; RNA interference.

OS Hepatitis B virus.
 XX US2003206887-A1.

PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0337055P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 09-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.

PA (MORR/) MORRISSEY D.
 PA (MCSW/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswiggen JA, Beigelman L;

DR WPI; 2003-901032/82.

XX New short interfering nucleic acid molecules which down-regulate
 PT expression of a hepatitis B virus (HBV) or which inhibit HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.

PS Claim 11, Page 48; 72pp; English.

XX The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX

SQ Sequence 19 BP; 7 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAAAGCA 16
 DB 3 AAAGCCACCCAAAGCA 18

RESULT 17
 ADL99637/C
 ID ADL99637 standard; RNA; 19 BP.

AC ADL99637;

DT 20-MAY-2004 (first entry)

DE Hepatitis B virus short interfering nucleic acid (siNA) #54.

KW siNA; hepatitis B virus; HBV; RNA interference.

OS Hepatitis B virus.
 XX US2003206887-A1.

PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

XX 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSW/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 XX
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 41; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises a sense
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises a sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 19 BP; 0 A; 4 C; 7 G; 0 T; 8 U; 0 Other;
 XX
 Query Match 100.0%; Score 16; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCACCAGGCA 16
 19 AAAGCACCAGGCA 4
 Db 19 AAAGCACCAGGCA 4
 RESULT 18
 ADM00161/c
 ID ADM00161 standard; RNA; 19 BP.
 XX
 AC ADM00161;
 XX
 DT 20-MAY-2004 (first entry)
 XX

DE Hepatitis B virus short interfering nucleic acid (siNA) #577.
 XX
 XX V-nucleide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
 KM siNA; hepatitis B virus; HBV, RNA interference.
 OS
 OS Hepatitis B virus.
 XX
 PN US2003206887-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 16-SEP-2002; 2002US-00244647.
 XX
 XX 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002MO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 XX
 PA (MORR/) MORRISSEY D.
 PA (MCSW/) MCSWIGGEN J A.
 PA (BEIG/) BEIGELMAN L.
 XX
 PI Morrissey D, Mcswigen JA, Beigelman L;
 XX
 DR WPI; 2003-901032/82.
 XX
 PT New short interfering nucleic acid molecules which down-regulates
 PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 PS Claim 11; Page 48; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises a sense
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises a sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural

CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.

CC Sequence 19 BP; 0 A; 3 C; 8 G; 0 T; 8 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 18 AAAGCCACCCAGGCA 3

RESULT 19
ADM00158/c
ADM00158 standard; RNA; 19 BP.

AC ADM00158;

DT 20-MAY-2004 (first entry)

DE Hepatitis B virus short interfering nucleic acid (siNA) #574.

KW siNA; Hepatitis B virus; HBV; RNA interference.

OS Hepatitis B virus.

PN US2003206887-A1.

PD 06-NOV-2003.

PF 16-SEP-2002; 2002US-00244647.

PR 14-MAY-1992; 92US-00882712.

PR 07-FEB-1994; 94US-00193627.

PR 08-NOV-1999; 99US-00436430.

PR 20-MAR-2000; 2000US-00531025.

PR 09-AUG-2000; 2000US-00636385.

PR 24-OCT-2000; 2000US-00696347.

PR 08-JUN-2001; 2001US-00877478.

PR 24-OCT-2001; 2001US-0296876P.

PR 05-DEC-2001; 2001US-0335059P.

PR 20-FEB-2002; 2002US-0337055P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PA (MORR/) MORRISSEY D.

PA (MCSW/) MCSWIGEN J A.

PA (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswigen JA, Beigelman L;

DR WPI; 2003-901032/82.

XX New short interfering nucleic acid molecules which down-regulate

PT expression of a hepatitis B virus (HBV) or which inhibits HBV

PT replication, useful for treating human HBV infections or for

PT characterizing gene function.

XX Claim 11; Page 48; 72pp; English.

XX The invention relates to a short interfering nucleic acid (siNA) molecule

CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA

CC interference or that inhibits HBV replication. Also disclosed are the

CC following: (i) a method of modulating the expression of a HBV gene in a

CC tissue explant; (ii) a method of generating a library of siNA constructs

CC having predetermined complexity; (iii) a cell containing one or more siNA
CC molecules; (iv) a kit containing a siNA molecule which can be used to
CC modulate the expression of a HBV target gene in a cell, tissue or
CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
CC molecule is adapted for use to treat HBV infection, and comprises a sense
CC complementary to an RNA sequence encoding HBV and the sense region
CC comprises sequence complementary to the antisense region. The siNA
CC molecule is assembled from 2 nucleic acid fragments, where one fragment
CC comprises the sense region and the second fragment comprises the
CC antisense region of the siNA molecule, where sense region and the
CC antisense region comprise separate oligonucleotides, and are covalently
CC connected via a linker molecule. The linker molecule is a polynucleotide
CC linker or a non-nucleotide linker. The sense region comprises a 3'-
CC terminal overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
CC The antisense region 3'-terminal overhang is complementary to RNA
CC encoding HBV. The siNA is useful for treating human hepatitis B virus
CC infections, and for characterizing pathways of gene function, e.g. to
CC inhibit activity of target genes in a pathway to determine the function
CC of uncharacterized genes in gene function analysis. The siNA molecules
CC may also be used in clinical, industrial, environmental, agricultural
CC and/or research settings. The present sequence represents 1 of 1504 HBV
CC siNA molecules of the invention.

Sequence 19 BP; 0 A; 3 C; 9 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 17 AAAGCCACCCAGGCA 2

RESULT 20
AAQ13771/c
AAQ13771 standard; DNA; 20 BP.

AC AAQ13771;

DT 25-MAR-2003 (revised)

DT 03-JAN-1992 (first entry)

DE HBV primer number 12.

XX Hepatitis B virus; ss.

XX Synthetic.

PN WO9114789-A.

PD 03-OCT-1991.

PF 28-MAR-1990; 90GB-00006924.

PR 28-MAR-1990; 90GB-00006924.

PA (UNIO) IMPERIAL COLLEGE SCI & TECHN.

PI Thomas H, Carman WF;

DR WPI; 1991-310588/42.

XX Predicting course of hepatitis B infection - by detecting viral strains

PT carrying specific mutation(s) more likely to cause fulminating

PT infections.

XX Disclosure; Page 3; 19pp; English.

XX The primer corresponds to positions 1877-1896 of HBV DNA. It is used to

CC detect the presence/absence of a pre-core variant of HB virus having the

CC mutation mu-1896 with or without mu-1899. The primer will detect only the
 CC negative HBV DNA strand with the mu-1896 mutation. See also AAQ13770-
 CC Q13773 (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 20 BP; 1 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 DB 19 AAAGCCACCCAGGCA 4

RESULT 21
 AAQ13772/c
 ID AAQ13772 standard; DNA; 20 BP.
 XX
 AC AAQ13772;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)
 XX
 DE HBV primer number 13.
 XX
 KM Hepatitis B virus; ss.
 XX
 OS Synthetic.
 XX
 PN WO9114789-A.
 XX
 PD 03-OCT-1991.
 XX
 PF 28-MAR-1990; 90GB-00006924.
 XX
 PR 28-MAR-1990; 90GB-00006924.
 XX
 PA (UNLO) IMPERIAL COLLEGE SCI & TECHN.
 XX
 PI Thomas H, Carman WF;
 XX
 DR WPI; 1991-310588/42.
 XX
 PT Predicting course of hepatitis B infection - by detecting viral strains
 PT carrying specific mutation(s) more likely to cause fulminating
 PT infections.
 XX
 PS Disclosure; Page 3; 199p; English.
 XX
 CC The primer corresponds to positions 1877-1896 of HBV DNA. It is used to
 CC detect the presence/absence of a pre-core variant of HB virus having the
 CC mutation mu-1896 with or without mu-1899. The primer will detect only the
 CC negative HBV DNA strand with neither mutation. See also AAQ13770-Q13773
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 20 BP; 0 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 DB 19 AAAGCCACCCAGGCA 4

RESULT 22
 AAQ85970
 ID AAQ85970 standard; DNA; 20 BP.
 XX
 AC AAQ85970;
 XX

DT 31-OCT-1995 (first entry)
 XX
 XX Hepatitis B virus polypeptide coding sequence primer p205.
 DE
 XX
 KM Hepatitis B virus; PCR; amplification; primer; antiviral agent; ss.
 XX
 OS Synthetic.
 XX
 PN JP07033797-A.
 XX
 PD 03-FEB-1995.
 XX
 PF 21-JUL-1993; 93JP-00180314.
 XX
 PR 21-JUL-1993; 93JP-00180314.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 DR WPI; 1995-110649/15.
 XX
 PT Polypeptide derived from hepatitis B virus and its coding gene. - may be
 PT used for detection of HBV not detectable by conventional methods.
 XX
 PS Example 2; Page 5; 7pp; Japanese.
 XX
 CC Primers AAQ85967-70 were used to PCR amplify the coding sequence for a
 CC polypeptide derived from hepatitis B virus (AAQ85966). The sequence
 CC encodes a polypeptide of 134 amino acids. The DNA was isolated from
 CC patients infected with hepatitis virus which was not detected by
 CC conventional methods. The polypeptide can be used in the diagnosis of
 CC hepatitis viral diseases which cannot be detected by conventional methods
 CC and in the development of antiviral agents
 XX

SQ Sequence 20 BP; 8 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 DB 3 AAAGCCACCCAGGCA 18

RESULT 23
 AAT70947
 ID AAT70947 standard; DNA; 20 BP.
 XX
 AC AAT70947;
 XX
 DT 27-OCT-1997 (first entry)
 XX
 DE HBV pre-genome element epsilon region antisense oligonucleotide.
 XX
 KM HBV; hepatitis B virus; S; surface antigen; C; core; P; polymerase;
 KM antisense; replication inhibition; hepatitis; infection; diagnosis;
 KM hepatocellular carcinoma; ss.
 XX
 OS Synthetic.
 XX
 PN WO9703211-A1.
 XX
 PD 30-JAN-1997.
 XX
 PF 26-JUN-1996; 96WO-US010984.
 XX
 PR 13-JUL-1995; 95US-00501968.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Anderson KP, Cowbert LM;
 XX
 DR WPI; 1997-119063/11.

XX New oligo:nucleotide(s) hybridisable with Hepatitis B virus RNA - used
 PT for inhibiting HBV replication and for diagnosis, treatment or prevention
 PT of HBV-associated diseases e.g. hepatitis.
 XX
 XX Claim 4, Page 16; 47pp; English.
 XX
 CC AAT70930-170969 are antisense oligonucleotides (ONs) capable of
 CC inhibiting the replication of hepatitis B virus (HBV). The ONs
 CC specifically hybridise to HBV RNA or pre-RNA which encodes a P (DNA
 CC polymerase), S (surface antigen) or C (core) gene product and/or with HBV
 CC ss RNA pre-genome elements e.g. 5' cap region, US region, epsilon region
 CC or a translation initiation site. The ONs can be used for diagnosing HBV
 CC infection, for inhibiting HBV replication and for treating or preventing
 CC a HBV associated diseases, e.g. acute, chronic or fulminant hepatitis or
 CC hepatocellular carcinoma
 CC
 SQ Sequence 20 BP; 8 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16
 RESULT 24
 ID AAQ92909 standard; cDNA; 21 BP.
 XX AAQ92909;
 XX 28-FEB-1996 (first entry)
 DT
 XX
 DE Antiviral oligonucleotide loop inhibits HBV replication.
 DE
 KM Replication; hepatitis virus; primer; DR11 region; hepatocyte; antiviral;
 KM herpes; influenza; drug; pre-S1 protein; polymerase; encapsidation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9519433-A2.
 PD 20-JUL-1995.
 XX
 PF 11-JAN-1995; 95WO-US000508.
 XX
 PR 12-JAN-1994; 94US-00181557.
 PR 08-AUG-1994; 94US-00287337.
 XX
 PA (TARG-) TARGETTECH INC.
 XX
 PI Carmichael E;
 PI
 PI
 PI
 PI
 DR WPI; 1995-263863/34.
 XX
 XX New oligo and polynucleotide(s) that inhibit viral replication -
 PT hybridise e.g. to an RNA primer or primer binding region, and their new
 PT soluble complexes, esp. for treating hepatitis B infection.
 PT
 XX
 PS Claim 20; Page 19; 31pp; English.
 PS
 CC Oligonucleotides AAQ92905-12 are used to inhibit the replication of
 CC hepatitis virus replication. This oligonucleotide binds to the cis-
 CC encapsidation signal of hepatitis B virus. The oligonucleotides are
 CC introduced into pref. hepatocytes, as soluble molecular complexes. They
 CC are used to treat hepatitis B virus infections but could also be used
 CC against e.g. Hepatitis A or C, herpes, influenza, etc. The
 CC oligonucleotides can also be used to detect the presence of the virus in
 CC a sample or to evaluate the effect of antiviral drugs
 CC
 CC

SQ Sequence 21 BP; 7 A; 10 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAGCCACCCAGGCA 16
 Db 6 AAAGCCACCCAGGCA 21
 RESULT 25
 ID AAT18255 standard; DNA; 21 BP.
 XX AAT18255;
 AC AAT18255;
 XX
 DT 17-SEP-1996 (first entry)
 XX
 DE HBV epsilon encapsidation mRNA intermediate antisense oligo L2b.
 DE
 XX
 KM Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
 KM epsilon; encapsidation; sequence; intermediate; subtype aw; C gene;
 KM treatment; chronic infection; modulation; translation; transcription;
 KM release; host cell; ss.
 XX
 OS Synthetic.
 XX
 PN WO9603152-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-US009143.
 XX
 PR 28-JUL-1994; 94US-00281106.
 XX
 PA (GEOU) UNIV GEORGETOWN.
 XX
 PI Korba BF, Gerin JL;
 PI
 PI
 DR WPI; 1996-116796/12.
 XX
 XX Single stranded oligo:nucleotide(s) for inhibiting replication of
 PT hepatitis B virus - are anti-sense to portions of the epsilon
 PT encapsidation sequence and modulate HBV function.
 PT
 XX
 PS Claim 14; Page 44; 56pp; English.
 PS
 CC The present sequence, which inhibits the replication of hepatitis B virus
 CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that
 CC binds the epsilon encapsidation sequence of a mRNA intermediate derived
 CC from the HBV genome. The 1st nucleotide of the oligonucleotide
 CC corresponds to nucleotide 1884 of the HBV aw subtype C gene, using the
 CC numbering scheme from the sequence published by Galibert et al., Nature
 CC 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to
 CC treat chronic HBV infection by modulating a HBV related function, e.g.
 CC translation, transcription, encapsidation, replication and release from a
 CC host cell. The effect of the oligonucleotide on the levels of HBV DNA in
 CC the extracellular medium (VIR. DNA), intracellular viral replicative
 CC intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface
 CC antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core
 CC antigen protein (HBcAg), given as the EC(90) (microm, 9 days of
 CC treatment) or ND (not determined), are VIR. DNA (11.8), HBV RI (ND), HBV
 CC RNA (ND), HBsAg (>20), HBeAg (>20) and HBcAg (18.8)
 CC
 SQ Sequence 21 BP; 8 A; 10 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 16; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAGCCACCCAGGCA 16
 Db 1 AAAGCCACCCAGGCA 16

Db 6 AAAGCCACCCAGCA 21

RESULT 26
 AAT18253
 ID AAT18253 standard; DNA; 21 BP.
 XX
 AC AAT18253;
 XX
 DT 17-SEP-1996 (first entry)
 XX
 DE HBV epsilon encapsidation mRNA intermediate antisense oligo L2.
 XX
 KM Inhibition; replication; hepatitis B virus; HBV; antisense; mRNA;
 KM epsilon; encapsidation; sequence; intermediate; subtype aye; C gene;
 KM treatment; chronic infection; modulation; translation; transcription;
 KM release; host cell; ss.
 XX
 OS Synthetic.
 XX
 PN MO9603152-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 28-JUL-1995; 95MO-US009143.
 XX
 PR 28-JUL-1994; 94US-00281106.
 XX
 PA (GEOU) UNIV GEORGETOWN.
 XX
 PI Korba BE, Gerin JL;
 XX
 DR WPI; 1996-116796/12.
 XX
 PT Single stranded oligo:nucleotide(s) for inhibiting replication of
 PT hepatitis B virus - are anti-sense to portions of the epsilon
 PT encapsidation sequence and modulate HBV function.
 XX
 PS Claim 12; Page 44; 56pp; English.
 XX
 CC The present sequence, which inhibits the replication of hepatitis B virus
 CC (HBV) in a host cell, is a single stranded antisense oligonucleotide that
 CC binds the epsilon encapsidation sequence of a mRNA intermediate derived
 CC from the HBV genome. The 1st nucleotide of the oligonucleotide
 CC corresponds to nucleotide 1879 of the HBV aye subtype C gene, using the
 CC numbering scheme from the sequence published by Galibert et al., Nature
 CC 281: 646 (1979). A compsn. comprising the oligonucleotide may be used to
 CC treat chronic HBV infection by modulating a HBV related function, e.g.
 CC translation, transcription, encapsidation, replication and release from a
 CC host cell. The effect of the oligonucleotide on the levels of HBV DNA in
 CC the extracellular medium (VIR. DNA), intracellular viral replicative
 CC intermediates (HBV RI), intracellular viral RNA (HBV RNA), HBV surface
 CC antigen protein (HBsAg), HBV e antigen protein (HBeAg) and HBV core
 CC antigen protein (HBcAg), given as the EC(90) (microm), 9 days of
 CC treatment or ND (not determined), are VIR. DNA (15.9), HBV RI (ND), HBV
 CC RNA (ND), HBsAg (>20), HBeAg (>20) and HBcAg (>20)
 XX
 SQ Sequence 21 BP; 8 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGCA 16
 |||||
 Db 1 AAAGCCACCCAGCA 16

RESULT 27
 AAT70936
 ID AAT70936 standard; DNA; 21 BP.
 XX
 AC AAT70936;

XX
 DT 27-OCT-1997 (first entry)
 XX
 DE HBV core gene antisense oligonucleotide.
 XX
 KM HBV; hepatitis B virus; S; surface antigen; C; core; P; polymerase;
 KM antisense; replication inhibition; hepatitis; infection; diagnosis;
 KM hepatocellular carcinoma; ss.
 XX
 OS Synthetic.
 XX
 PN MO9703211-A1.
 XX
 PD 30-JAN-1997.
 XX
 PF 26-JUN-1996; 96MO-US010984.
 XX
 PR 13-JUL-1995; 95US-00501968.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Anderson KP, Cowbert LM;
 XX
 DR WPI; 1997-119063/11.
 XX
 PT New oligo:nucleotide(s) hybridizable with Hepatitis B virus RNA - used
 PT for inhibiting HBV replication and for diagnosis, treatment or prevention
 PT of HBV-associated diseases e.g. hepatitis.
 XX
 PS Example 1; Page 16; 47pp; English.
 XX
 CC AAT70930-T70969 are antisense oligonucleotides (ONs) capable of
 CC inhibiting the replication of hepatitis B virus (HBV). The ONs
 CC specifically hybridize to HBV RNA or pre-RNA which encodes a P (DNA
 CC polymerase), S (surface antigen) or C (core) gene product and/or with HBV
 CC ss RNA pre-genome elements e.g. a 5' cap region, US region, epsilon
 CC region or a translation initiation site. The ONs can be used for
 CC diagnosing HBV infection, for inhibiting HBV replication and for treating
 CC or preventing a HBV associated disease, e.g. acute, chronic or fulminant
 CC hepatitis or hepatocellular carcinoma
 XX
 SQ Sequence 21 BP; 8 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGCA 16
 |||||
 Db 3 AAAGCCACCCAGCA 18

RESULT 28
 ADA13842/c
 ID ADA13842 standard; RNA; 21 BP.
 XX
 AC ADA13842;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:179.
 XX
 KM double-stranded short interfering nucleic acid;
 KM short interfering nucleic acid; siNA; expression; replication;
 KM inhibition; RNA interference; virucide; anti-HIV; hepatocytic;
 KM antiinflammatory; plant; antiviral; vasotrophic; neuroprotective;
 KM cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotoxic;
 KM endocrine; viral infection; hepatitis B; hepatitis C; HIV;
 KM herpes simplex; cytomegalovirus; human papillomavirus;
 KM respiratory syncytial virus; influenza virus; reseasons;
 KM neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
 KM pulmonary; renal; liver; mitochondrial; reproductive disease;
 KM chemical modification; ss.

XX OS Synthetic.
 XX PN WO2003070918-A2.
 XX XX 28-AUG-2003.
 XX PD 20-FEB-2003; 2003WO-US005346.
 XX PF 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX PR 15-JAN-2003; 2003US-0440129P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI McSwiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
 XX PT Morrissey D, Fosenbaugh K, Mokler V, Jamison S;
 XX PT WPI; 2003-689785/65.
 XX PT New short interfering nucleic acid containing no ribonucleotides, useful
 XX PT e.g. for treating viral infection, downregulates expression of target
 XX PT gene or RNA.
 XX PS Example 4; Page 137; 204pp; English.
 XX XX The present invention describes a double-stranded short interfering
 XX CC nucleic acid (siNA) that downregulates expression of a target gene, where
 XX CC the siNA molecule comprises no ribonucleotides and each strand of the
 XX CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)
 XX CC a siNA molecule that inhibits expression of target RNA; (2) a siNA
 XX CC molecule that inhibits replication of a virus and optionally does not
 XX CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule
 XX CC that inhibits expression of a target gene and does not require presence
 XX CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits
 XX CC expression of a target gene by mediating RNA interference; and (5) a
 XX CC method for modulating expression of a gene in a cell using siNA
 XX CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,
 XX CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,
 XX CC cytosstatic, cardiovascular, immunosuppressive, respiratory, nephrotoxic
 XX CC and endocrine activities. The siNA's are useful for downregulating
 XX CC expression of target genes, inhibiting expression of target RNA, and
 XX CC inhibiting replication of a virus. siNA molecules can be used: (a) for
 XX CC therapy of any disorder that responds to modulation of gene expression,
 XX CC especially animal and plant viral infections, specifically hepatitis B or
 XX CC C, HIV; herpes simplex; cytomegalo; human papilloma; respiratory
 XX CC syncytial or influenza viruses, and also many other diseases such as
 XX CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
 XX CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
 XX CC endocrine or reproductive diseases; and (b) for diagnosis, target
 XX CC validation, genomic discovery, genetic engineering, pharmacogenomics and
 XX CC analysis of gene function. Chemical modification of siNA molecules
 XX CC improves interfering activity; stability; cellular uptake; binding
 XX CC affinity and/or mediates increased polymerase activity. siNA may be
 XX CC designed to target many related genes containing a conserved sequence.
 XX CC The present sequence represents a siNA oligonucleotide sequence, which is
 XX CC used in the exemplification of the present invention.
 XX XX Sequence 21 BP; 1 A; 4 C; 8 G; 2 T; 6 U; 0 Other;
 XX XX
 QY Best Local Match 100.0%; Score 16; DB 9; Length 21;
 QY Query Similarity 100.0%; Pred. NO. 9.5;
 Db Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AAAGCACCACCAAGCA 16
 21 AAAGCACCACCAAGCA 6

RESULT 29
 ADM00924/C
 ID ADM00924 standard; RNA; 21 BP.
 XX AC ADM00924;
 XX XX 20-MAY-2004 (first entry)
 XX DT 20-MAY-2004 (first entry)
 XX XX Hepatitis B virus short interfering nucleic acid (siNA) #1340.
 XX DE Hepatitis B virus short interfering nucleic acid (siNA) #1340.
 XX XX siNA; hepatitis B virus; HBV, RNA interference.
 XX OS Hepatitis B virus.
 XX EN US2003206887-A1.
 XX PD 06-NOV-2003.
 XX PF 16-SEP-2002; 2002US-00244647.
 XX PR 14-MAY-1992; 92US-00882712.
 XX PR 07-FEB-1994; 94US-00193627.
 XX PR 08-NOV-1999; 99US-00436430.
 XX PR 20-MAR-2000; 2000US-00531025.
 XX PR 09-AUG-2000; 2000US-00636385.
 XX PR 24-OCT-2000; 2000US-00696347.
 XX PR 08-JUN-2001; 2001US-00877478.
 XX PR 08-JUN-2001; 2001US-0296876P.
 XX PR 24-OCT-2001; 2001US-035059P.
 XX PR 05-DEC-2001; 2001US-0337055P.
 XX PR 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 26-MAR-2002; 2002WO-US00918P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX PA (MORR/) MORRISSEY D.
 XX PA (MCSW/) MCSWIGGEN J A.
 XX PA (BEIG/) BEIGELMAN L.
 XX PI Morrissey D, McSwiggen JA, Beigelman L;
 XX PT WPI; 2003-901032/82.
 XX PT New short interfering nucleic acid molecules which down-regulates
 XX PT expression of a hepatitis B virus (HBV) or which inhibits HBV
 XX PT replication, useful for treating human HBV infections or for
 XX PT characterizing gene function.
 XX PS Claim 11; Page 51; 72pp; English.
 XX XX The invention relates to a short interfering nucleic acid (siNA) molecule
 XX CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 XX CC interference or that inhibits HBV replication. Also disclosed are the
 XX CC following: (i) a method of modulating the expression of a HBV gene in a
 XX CC tissue explant; (ii) a method of generating a library of siNA constructs
 XX CC having predetermined complexity; (iii) a cell containing one or more siNA
 XX CC molecules; (iv) a kit containing a siNA molecule which can be used to
 XX CC modulate the expression of a HBV target gene in a cell, tissue or
 XX CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 XX CC molecule is adapted for use to treat HBV infection, and comprises a sense
 XX CC and an antisense region, where the antisense region comprises sequence
 XX CC complementary to an RNA sequence encoding HBV and the sense region
 XX CC comprises sequence complementary to the antisense region. The siNA
 XX CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 XX CC comprises the sense region and the second fragment comprises the
 XX CC antisense region of the siNA molecule, where sense region and the
 XX CC antisense region comprise separate oligonucleotides, and are covalently
 XX CC connected via a linker molecule. The linker molecule is a polynucleotide
 XX CC linker or a non-nucleotide linker. The sense region comprises a 3'-

CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterising pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.

SQ Sequence 21 BP; 1 A; 4 C; 8 G; 2 T; 6 U; 0 Other;

Query Match 100.0%; Score 16; DB 11; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Gaps 0;

QY 1 AAAGCCACCCCAAGGCA 16
 Db 21 AAAGCCACCCCAAGGCA 6

RESULT 30
 ID AAQ13770/c
 XX AAQ13770 standard; DNA; 23 BP.

AC AAQ13770;

DT 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)

DE HBV primer number 11.

KM Hepatitis B virus; ss.

OS Synthetic.

PN MO9114789-A.

PD 03-OCT-1991.

PF 28-MAR-1990; 90GB-00006924.

PR 28-MAR-1990; 90GB-00006924.

PA (UNLO) IMPERIAL COLLEGE SCI & TECHN.

PI Thomas H, Garman WF;

WPI; 1991-310588/42.

PT Predicting course of hepatitis B infection - by detecting viral strains
 PT carrying specific mutation(s) more likely to cause fulminating
 PT infections.

PS Disclosure; Page 3; 19pp; English.

CC The primer corresponds to positions 1877-1899 of HBV DNA. It is used to
 CC detect the presence/absence of a pre-core variant of HB virus having the
 CC mutation mu-1896 with or without mu-1899. The primer will detect only the
 CC negative HBV DNA strand with both the mutations. See also AAQ13771-Q13773
 CC (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 23 BP; 2 A; 4 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 23;

Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Gaps 0;

QY 1 AAAGCCACCCCAAGGCA 16
 Db 19 AAAGCCACCCCAAGGCA 4

RESULT 31
 ID AAT03266/c
 XX AAT03266 standard; DNA; 23 BP.

AC AAT03266;

DT 02-APR-1996 (first entry)

DE Hepatitis B virus (HBV) sense primer OAL41.

KM Polymerase chain reaction; PCR; primer; amplify; hepatitis B virus; HBV;
 KM prec; S gene; diagnosis; ss.

OS Synthetic.

PN JP07203972-A.

PD 08-AUG-1995.

PF 07-JAN-1994; 94JP-00000515.

PR 07-JAN-1994; 94JP-00000515.

PA (SAGA) OTSUKA PHARM CO LTD.

WPI; 1995-307167/40.

PT Hepatitis B virus DNA fragment contg. S gene region and mutant prec
 PT region - useful for simultaneous detection of mutant and complete HBV DNA
 PT for diagnosis of hepatitis B.

PS Example 1; Col 7; 10pp; Japanese.

CC The sequences represented by AAT03266-T03272 are amplification primers
 CC for Hepatitis B virus DNA fragments containing the S gene region and the
 CC mutant prec region. This sequence corresponds to nucleotides 1748-1770 of
 CC HBV-DNA. The mutant prec region produces no HBe antigen and contains a
 CC point mutation (G83 to A83). The DNA fragments can be used for a
 CC simultaneous determination of a mutant HBV-DNA and a total HBV-DNA. This
 CC can be used to diagnose hepatitis B

SQ Sequence 23 BP; 3 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 23;

Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Gaps 0;

QY 1 AAAGCCACCCCAAGGCA 16
 Db 22 AAAGCCACCCCAAGGCA 7

RESULT 32
 ID AAQ81424/c
 XX AAQ81424 standard; DNA; 23 BP.

AC AAQ81424;

DT 25-MAR-2003 (revised)

DT 13-AUG-1995 (first entry)

DE HBV hybridization probe.

KM HBV; hepatitis B virus; hybridization; probe; detection; PCR;
 KM polymerase chain reaction; LCR; ligase chain reaction; ss.

OS Synthetic.

PN MO9502690-A1.

PD 26-JAN-1995.

PF 08-JUL-1994; 94MO-US007684.
XX
PR 13-JUL-1993; 93US-00090755.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Spies U;
XX
DR WPI; 1995-067334/09.
XX
PT Novel composition containing ligation incompetent upstream and downstream
XX probes - for the detection of hepatitis B virus.
PS Disclosure; Page 45; 70pp; English.
XX
CC Probes given in AAQ81412-31 and AAQ81437-44 are used to detect hepatitis
CC B virus (HBV) in test samples. The probes, which include ligation
CC incompetent upstream and downstream probes that can be corrected by a gap
CC -fill or exo format, and which can be used in PCR and LCR protocols,
CC hybridize to target sequences of HBV, selected from those given in
CC AAQ81432-36. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 23 BP; 2 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCCACCCCAAGGCA 16
DB 23 AAAGCCACCCCAAGGCA 8

RESULT 33
AAD19005/C
ID AAD19005 standard; DNA; 23 BP.
AC AAD19005;
XX
DT 18-DEC-2001 (first entry)
XX
DE Hepatitis B virus (HBV) precore DNA amplifying forward PCR primer #5.
XX
KM Hepatitis B virus; HBV; bacterial infection; fungi; protozoa; PCR primer;
KM amplification; blood-borne pathogen; sexually transmitted disease;
KM respiratory disease; ss.
OS Hepatitis B virus.
XX
PN WO200168921-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001MO-US008110.
XX
PR 14-MAR-2000; 2000US-0189344P.
XX
PA (INVE-) INVESTIGEN.
XX
PI Koshinsky H, Zwick MS, McCue KF;
XX WPI; 2001-611396/70.
XX
DR Simultaneous detection of biological entities such as bacteria, fungi and
XX viruses by specific nucleic acid amplification.
PT
PS Disclosure; Page 31; 55pp; English.

XX The invention relates to a method and apparatus for the simultaneous
CC detection of multiple biological entities such as bacteria, fungi and
CC viruses by specific nucleic acid amplification. The invention also
CC relates to a kit for simultaneous detection of biological entities. The
CC kit is employed for detecting blood-borne pathogens, associated with a

CC variety of infectious diseases such as respiratory and sexually
CC transmitted diseases. The methods and apparatus are used for the
CC simultaneous detection of biological entities present in biological and
CC environment samples. In particular, they are used for monitoring diseases
CC cause by microorganisms associated with a respiratory or sexually
CC transmitted disease such as a bacterium (staphylococcus, pneumococcus,
CC gonococcus, haemophilus, bacteroides, bacterioids or salmonella), virus
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,
CC HDV, HEV, HGV or TTV), fungus (aspergillus fumigatus, blastomycosis,
CC dermatitis, candida albicans) or protozoa (Entamoeba histolytica). The
CC present sequence is a PCR primer used for amplifying Hepatitis B Virus
XX (HBV) precore DNA
XX
SQ Sequence 23 BP; 2 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCCACCCCAAGGCA 16
DB 23 AAAGCCACCCCAAGGCA 8

RESULT 34
ADM00880/C
ID ADM00880 standard; RNA; 23 BP.
AC ADM00880;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hepatitis B virus short interfering nucleic acid (siNA) #1296.
XX
KM Virucide; Hepatotropic; Gene therapy; ss; short interfering nucleic acid;
KM siNA; hepatitis B virus; HBV; RNA interference.
XX
OS Hepatitis B virus.
XX
PN US2003206887-A1.
XX
PD 06-NOV-2003.
XX
PF 16-SEP-2002; 2002US-00244647.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00511025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
PR 24-OCT-2001; 2001US-0296876P.
PR 05-DEC-2001; 2001US-0335059P.
PR 20-FEB-2002; 2002US-0337055P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002MO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

XX (MORR/) MORRISSEY D.
XX (MCSW/) MCSWIGGEN J A.
XX (BEIG/) BEIGELMAN L.

PI Morrissey D, Mcswiggen JA, Beigelman L;
XX WPI; 2003-901032/82.
XX
DR New short interfering nucleic acid molecules which down-regulates
XX expression of a hepatitis B virus (HBV) or which inhibits HBV
PT

PT replication, useful for treating human HBV infections or for
 PT characterizing gene function.
 XX
 XX
 PS Claim 11; Page 51; 72pp; English.
 XX
 CC The invention relates to a short interfering nucleic acid (siNA) molecule
 CC that down-regulates expression of a hepatitis B virus (HBV) gene by RNA
 CC interference or that inhibits HBV replication. Also disclosed are the
 CC following: (i) a method of modulating the expression of a HBV gene in a
 CC tissue explant; (ii) a method of generating a library of siNA constructs
 CC having predetermined complexity; (iii) a cell containing one or more siNA
 CC molecules; (iv) a kit containing a siNA molecule which can be used to
 CC modulate the expression of a HBV target gene in a cell, tissue or
 CC organism; and (v) a method for synthesizing a siNA molecule. The siNA
 CC molecule is adapted for use to treat HBV infection, and comprises a sense
 CC and an antisense region, where the antisense region comprises sequence
 CC complementary to an RNA sequence encoding HBV and the sense region
 CC comprises sequence complementary to the antisense region. The siNA
 CC molecule is assembled from 2 nucleic acid fragments, where one fragment
 CC comprises the sense region and the second fragment comprises the
 CC antisense region of the siNA molecule, where sense region and the
 CC antisense region comprise separate oligonucleotides, and are covalently
 CC connected via a linker molecule. The linker molecule is a polynucleotide
 CC linker or a non-nucleotide linker. The sense region comprises a 3'-terminal
 CC terminal overhang and the antisense region comprises a 3'-terminal
 CC overhang. The 3'-terminal overhangs each comprise about 2 nucleotides.
 CC The antisense region 3'-terminal overhang is complementary to RNA
 CC encoding HBV. The siNA is useful for treating human hepatitis B virus
 CC infections, and for characterizing pathways of gene function, e.g. to
 CC inhibit activity of target genes in a pathway to determine the function
 CC of uncharacterised genes in gene function analysis. The siNA molecules
 CC may also be used in clinical, industrial, environmental, agricultural
 CC and/or research settings. The present sequence represents 1 of 1504 HBV
 CC siNA molecules of the invention.
 XX
 SQ Sequence 23 BP; 2 A; 5 C; 8 G; 0 T; 8 U; 0 Other;
 XX
 Query Match 100.0%; Score 16; DB 11; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 23 AAAGCCACCCAGGCA 8
 XX
 RESULT 35
 ID AAV29303/c
 AC AAV29303; standard; DNA; 30 BP.
 XX
 AC AAV29303;
 XX
 DT 27-AUG-2003 (revised)
 DT 29-JUL-1998 (first entry)
 XX
 DE Hepatitis B virus (HBV) core fragment DNA amplifying primer 3.
 XX
 KM Hepatitis B virus; HBV; vaccine; treatment; viral infection;
 KM hepatitis infection; PCR primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN WO9811916-A1.
 XX
 PD 26-MAR-1998.
 XX
 PF 18-SEP-1997; 97MO-US016541.
 XX
 PR 18-SEP-1996; 96US-0026313P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX

PI Shih C, Yuan T;
 XX
 DR WPI; 1998-217032/19.
 XX
 PT Defective interfering virus particle that occurs naturally in infection -
 PT used in protective vaccines and for treating viral, specifically
 PT hepatitis B, infections.
 XX
 PS Example 1; Page 23; 84pp; English.
 XX
 CC This primer is used for the PCR amplification of the Hepatitis B virus
 CC (HBV) DNA. This is used for the detection of a core deleted variant found
 CC in HBV infections. A defective, interfering virus particle that occurs
 CC naturally in a human infection has been identified. The invention
 CC provides a vector comprising a DNA sequence encoding the defective virus
 CC particle and origin of replication and a promoter/enhancer element. Host
 CC cells transformed with this vector can produce this defective virus
 CC particle which is useful in vaccines (of live virus or subunit types),
 CC particularly against HBV infection, including use in babies born to
 CC mothers who are not HBV carriers (particularly administered together with
 CC HBV-specific immunoglobulin). The defective interfering virus particle
 CC can also be used to treat infections, especially fulminant, chronic or
 CC acute hepatitis. Since the defective particle is almost identical to
 CC fully infectious virus, it should produce a stronger, more effective and
 CC longer-lasting protection against HBV than known subunit vaccines based
 CC on surface antigen only, with a lower failure rate. (Updated on 27-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 30 BP; 5 A; 5 C; 10 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 16; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGCCACCCAGGCA 16
 Db 30 AAAGCCACCCAGGCA 15
 XX
 RESULT 36
 ID AAS14628/c
 AC AAS14628;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE NASBA molecular beacon probe MB WT 1.
 XX
 KM NASBA; nucleic acid sequence based amplification; ss; probe;
 KM anchor sequence; anti-viral; hepatitis B virus; HBV; HBV infection;
 KM isothermal continuous transcription based amplification; WT 1.
 XX
 OS Hepatitis B virus.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT FT
 FT modified_base 32
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "DABCYL (not defined) labelled as a quencher"
 XX
 PN WO200164959-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001MO-EP002143.
 XX
 PR 02-MAR-2000; 2000EP-00200737.
 XX


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PA (ALKU ) AKZO NOBEL NV.
XX
XX Goudamit J, Yates SC, Penning MT, Van De Weijer LHM,
XX
XX WPI; 2001-602572/68.
XX
PT Monitoring anti-viral therapy, where hepatitis B virus (HBV) mRNA is
PT detected, useful for monitoring the efficacy of HBV treatment, by
PT amplifying a target nucleic acid in a sample obtained from a subject
XX
XX suspected of HBV infection.
XX
PS Example 6; Page 12; 42pp; English.
XX
CC The invention relates to monitoring anti-viral therapy, where hepatitis B
CC virus (HBV) mRNA is detected, comprising amplifying a target nucleic acid
CC sequence in a sample, which is obtained from an individual suspected of
CC HBV infection, using at least one oligonucleotide primer and
CC amplification reagents. The amplification method is preferably NASBA
CC (nucleic acid sequence based amplification) which is an isothermal
CC continuous transcription based amplification method. The method is useful
CC for monitoring anti-viral therapy, where HBV is detected. In particular,
CC the method is useful for monitoring the efficacy of the treatment. Prior
CC methods are either based on immunologic markers or the detection of the
CC HBV DNA in virus particles. The present method actually directly measures
CC the replication of the virus and immediately indicates the emergence of
CC resistant virus strains. The present method also provides insight into
CC how to interpret the results in order to predict the outcome of the
CC therapy. Thus, a more efficient therapy can be given to the patient
CC concerned. The present sequence is a NASBA molecular beacon probe for use
CC in the method of the invention.
XX
SQ Sequence 32 BP; 2 A; 7 C; 14 G; 9 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 16; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AAAGCCACCCCAAGCA 16
Db 22 AAAGCCACCCCAAGCA 7
XX
RESULT 37
AAT71784/c
ID AAT71784 standard; DNA; 44 BP.
XX
AC AAT71784;
XX
DT 29-AUG-1997 (first entry)
XX
DE Hepatitis B virus precore antigen target sequence mutant.
XX
KM HBV, ligase chain reaction; internal standard; amplification; ds.
XX
OS Hepatitis B virus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 19 /*tag= a
FT /*tag= b
FT misc_difference 21 /*tag= "G in wild-type"
FT /*tag= "G in wild-type"
XX
XX MO9640996-A1.
XX
PD 19-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008429.
XX
PR 07-JUN-1995; 95US-00480220.
XX

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PA (ABBO ) ABBOTT LAB.
XX
XX Birkenmeyer L, Mushahwar IK;
XX
XX WPI; 1997-052367/05.
XX
XX
PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT virus - can distinguish wild-type and mutant DNA types.
XX
XX Claim 13; Page 29; 40pp; English.
XX
CC A novel method has been produced for detecting the amount of a target
CC nucleic acid sequence which may be present in a test sample. It involves
CC contacting the test sample with means for performing a nucleic acid
CC amplification reaction; and determining the ratio of target amplification
CC products to internal standard amplification products present in the
CC sample. The present sequence represents a target sequence from hepatitis
CC B virus (HBV) precore antigen (mutant). The method can be used for
CC distinguishing between two different nucleic acid sequences present in a
CC sample, e.g. wild-type and mutant. The compositions can be used for
CC quantitatively detecting the DNA of HBV
XX
SQ Sequence 44 BP; 10 A; 8 C; 12 G; 14 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 16; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AAAGCCACCCCAAGCA 16
Db 18 AAAGCCACCCCAAGCA 3
XX
RESULT 38
AAT71783/c
ID AAT71783 standard; DNA; 44 BP.
XX
AC AAT71783;
XX
DT 29-AUG-1997 (first entry)
XX
DE Hepatitis B virus precore antigen target sequence wild-type.
XX
KM HBV, ligase chain reaction; internal standard; amplification; ds.
XX
OS Hepatitis B virus.
XX
PN WO9640996-A1.
XX
PD 19-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008429.
XX
PR 07-JUN-1995; 95US-00480220.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Birkenmeyer L, Mushahwar IK;
XX
XX WPI; 1997-052367/05.
XX
XX
PT Quantitative detection of target nucleic acid sequence, esp. hepatitis B
PT virus - can distinguish wild-type and mutant DNA types.
XX
XX Claim 13; Page 29; 40pp; English.
XX
CC A novel method has been produced for detecting the amount of a target
CC nucleic acid sequence which may be present in a test sample. It involves
CC contacting the test sample with means for performing a nucleic acid
CC amplification reaction; and determining the ratio of target amplification
CC products to internal standard amplification products present in the
CC sample. The present sequence represents a target sequence from hepatitis
CC B virus (HBV) precore antigen (wild-type). The method can be used for

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CC distinguishing between two different nucleic acid sequences present in a
 CC sample e.g. wild-type and mutant. The compositions can be used for
 CC quantitatively detecting the DNA of HBV

SO Sequence 44 BP; 8 A; 8 C; 14 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGCA 16
 DB 18 AAGCCACCCAGGCA 3

RESULT 39
 ABK14698/C
 ID ABK14698 standard; RNA; 48 BP.

AC ABK14698;
 DT 08-MAY-2002 (first entry)

XX HBV encapsidation signal target sequence #1.

KW Encapsidation signal; epsilonRNA; virucide; hepatotropic;
 KW antiinflammatory; hepatitis B virus; infection; chicken pox;
 KW 1,3,5-triazine derivative; DNA virus; RNA virus; gastroenteritis;
 KW infectious mononucleosis; smallpox; allergic rash; aseptic meningitis;
 KW influenza; acquired immune deficiency syndrome; AIDS; measles; ss.
 XX Hepatitis B virus.

XX Key Location/Qualifiers
 FH misc_binding 6..9

FT /*tag= a
 /bound_moiety= "Binds nucleotides 48-45 of the present
 sequence"
 FT 16..20

FT /*tag= b
 /bound_moiety= "Binds nucleotides 44-40 of the present
 sequence"
 FT 22..37

FT /*tag= d
 40..44
 FT /*tag= e
 /bound_moiety= "Binds nucleotides 20-16 of the present
 sequence"
 FT 45..48

FT /*tag= f
 /bound_moiety= "Binds nucleotides 9-6 of the present
 sequence"
 FT 45..48

PN USG335339-BI.

PD 01-JAN-2002.

PF 13-JAN-1999; 99US-00229703.

PR 13-JAN-1998; 98US-0006430.
 PR 13-JAN-1998; 98US-0113656P.

PA (SCRI-) SCRIPTGEN PHARM INC.

PI Arenas JE, Cload ST, Fleming ES, Xiang YB,

DR WPI; 2000-022911/02.

PT Pharmaceutical formulations for treating HBV and microbial infections and
 PT detecting target nucleic acids.

PS Disclosure; Fig 255B, 114pp; English.

CC This invention relates to a novel method for the treatment or prevention
 CC of viral infection such as hepatitis B virus infection in a patient. The
 CC method involves administering substituted 1,3,5-triazine derivatives or
 CC their salts to the patient. These triazine derivatives bind to and
 CC inhibit functional nucleic acids and as such may be used to treat many
 CC DNA and RNA viruses. The method of the invention may be used as a
 CC Hepatitis B virus (HBV) replication inhibitor and is useful for the
 CC treatment or prevention of viral infection, such as hepatitis B virus
 CC infection, gastroenteritis, chicken pox, infectious mononucleosis,
 CC smallpox, allergic rash, aseptic meningitis, influenza, acquired immune
 CC deficiency syndrome (AIDS), measles and many other diseases listed in the
 CC specification. The methods of the invention can also be used for treating
 CC diseases associated with deoxyribonucleic acid and ribonucleic acid, for
 CC detection and/or purification of nucleic acids. The present sequence
 CC represents a target sequence used in an example of the method of the
 CC invention comprising a region of the HBV encapsidation signal
 CC (epsilonRNA). This sequence is important for the encapsidation of the
 CC pregenome into virus and is also thought to play a role in activation of
 CC the HBV encoded polymerase

SO Sequence 48 BP; 8 A; 12 C; 15 G; 0 T; 13 U; 0 Other;

Query Match 100.0%; Score 16; DB 3; Length 48;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGCA 16
 DB 45 AAGCCACCCAGGCA 30

RESULT 40
 ABK14696/C
 ID ABK14696 standard; RNA; 48 BP.

AC ABK14696;

DT 08-MAY-2002 (first entry)

XX RNA target region comprising HBV encapsidation signal.

KW Encapsidation signal; epsilonRNA; virucide; hepatotropic;
 KW antiinflammatory; hepatitis B virus; infection; chicken pox;
 KW 1,3,5-triazine derivative; DNA virus; RNA virus; gastroenteritis;
 KW infectious mononucleosis; smallpox; allergic rash; aseptic meningitis;
 KW influenza; acquired immune deficiency syndrome; AIDS; measles; ss.
 XX Hepatitis B virus.

XX Key Location/Qualifiers
 FH misc_binding 6..9

FT /*tag= a
 /bound_moiety= "Binds nucleotides 48-45 of the present
 sequence"
 FT 16..20

FT /*tag= b
 /bound_moiety= "Binds nucleotides 44-40 of the present
 sequence"
 FT 22..26

FT /*tag= c
 /bound_moiety= "Binds nucleotides 38-33 of the present
 sequence"
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FT /*tag= d
 /bound_moiety= "Binds nucleotides 26-22 of the present
 sequence"
 FT 40..44

FT /*tag= e
 /bound_moiety= "Binds nucleotides 20-16 of the present
 sequence"
 FT 45..48

FT /*tag= f
 /bound_moiety= "Binds nucleotides 9-6 of the present
 sequence"
 FT 45..48

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FT      sequence "
XX      US6335339-B1.
PN      01-JAN-2002.
XX      13-JAN-1999; 99US-00229703.
XX      13-JAN-1998; 98US-00006430.
PR      13-JAN-1998; 98US-0113656P.
XX      (SCRI-) SCRIPGEN PHARM INC.
XX      Arenas JE, Cload ST, Fleming ES, Xiang YB;
PI      WPI; 2000-022911/02.
DR      Pharmaceutical formulations for treating HBV and microbial infections and
XX      detecting target nucleic acids.
PT      Example 2; Fig 258B; 114pp; English.
XX      This invention relates to a novel method for the treatment or prevention
XX      of viral infection such as hepatitis B virus infection in a patient. The
XX      method involves administering substituted 1,3,5-triazine derivatives or
XX      their salts to the patient. These triazine derivatives bind to and
XX      inhibit functional nucleic acids and as such may be used to treat many
XX      DNA and RNA viruses. The method of the invention may be used as a
XX      Hepatitis B virus (HBV) replication inhibitor and is useful for the
XX      treatment or prevention of viral infection, such as hepatitis B virus
XX      infection, gastroenteritis, chicken pox, infectious mononucleosis,
XX      smallpox, allergic rash, aseptic meningitis, influenza, acquired immune
XX      deficiency syndrome (AIDS), measles and many other diseases listed in the
XX      specification. The methods of the invention can also be used for treating
XX      diseases associated with deoxyribonucleic acid and ribonucleic acid, for
XX      detection and/or purification of nucleic acids. The present sequence
XX      represents a target sequence used in an example of the method of the
XX      invention comprising the HBV encapsidation signal (EpsilonRNA). This
XX      sequence is important for the encapsidation of the pregenome into virus
XX      and is also thought to play a role in activation of the HBV encoded
XX      polymerase
SQ      Sequence 48 BP; 8 A; 12 C; 15 G; 0 T; 13 U; 0 Other;
      Query Match 100.0%; Score 16; DB 3; length 48;
      Best Local Similarity 100.0%; Pred. No. 9.4;
      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AAAGCCACCCAGGCA 16
      |||||
Db      45 AAAGCCACCCAGGCA 30

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OM nucleic - nucleic search, using sw model

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and is derived by analysis of the total score distribution.

SUMMARIES

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C 34	16	100.0	114	3	US-08-075-520A-8	Sequence 11, Appl
C 35	16	100.0	291	3	US-08-075-520A-11	Sequence 16, Appl
C 36	16	100.0	390	3	US-08-075-520A-16	Sequence 2, Appl
C 37	16	100.0	477	3	US-08-445-585-2	Sequence 4, Appl
C 38	16	100.0	534	3	US-08-075-520A-4	Sequence 5, Appl
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C 40	16	100.0	558	3	US-08-075-520A-35	Sequence 56, Appl
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C 42	16	100.0	655	5	PCT-US93-01009-56	Sequence 42, Appl
C 43	16	100.0	909	3	US-09-243-282-1	Sequence 30, Appl
C 44	16	100.0	2348	3	US-08-480-173A-42	Sequence 14, Appl
C 45	16	100.0	2348	3	US-08-484-408A-42	Sequence 30, Appl
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107	14	87.5	601	4	US-09-949-016-91519	Sequence 91519, A	C 180	13	81.2	699	4	US-09-248-796A-282	Sequence 2822, Ap
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C 112	14	87.5	601	4	US-09-949-016-14634	Sequence 14634, A	C 185	13	81.2	1318	4	US-09-949-016-4189	Sequence 4189, Ap
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116	14	87.5	3728	1	US-08-111-939-1	Sequence 1, Appl	C 189	13	81.2	1873	4	US-09-770-767-12062	Sequence 12062, A
117	14	87.5	3935	3	US-09-060-489-1	Sequence 1, Appl	C 190	13	81.2	2088	4	US-09-248-796A-6792	Sequence 6792, Ap
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C 120	14	87.5	6435	4	US-09-949-016-2884	Sequence 2884, Ap	C 193	13	81.2	2209	4	US-09-949-016-4507	Sequence 4507, App
C 121	14	87.5	6435	4	US-09-949-016-2885	Sequence 2885, Ap	C 194	13	81.2	2212	4	US-09-919-497-25	Sequence 25, Appl
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124	14	87.5	13104	3	US-08-256-799-4	Sequence 4, Appl	C 197	13	81.2	3619	4	US-09-919-039-212	Sequence 3496, Ap
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C 127	14	87.5	21914	4	US-09-949-016-14626	Sequence 14626, A	C 200	13	81.2	4403	2	US-08-447-64-1	Sequence 1, Appl
C 128	14	87.5	21914	4	US-09-949-016-14627	Sequence 14627, A	C 201	13	81.2	4403	3	US-09-336-503-1	Sequence 1, Appl
C 129	14	87.5	21914	4	US-09-949-016-14732	Sequence 14732, A	C 202	13	81.2	4403	3	US-09-949-016-369	Sequence 369, App
C 130	14	87.5	21914	4	US-09-949-016-14733	Sequence 14733, A	C 203	13	81.2	4403	5	PCT-US93-02147A-1	Sequence 1, Appl
131	14	87.5	31063	4	US-09-596-002-20	Sequence 20, Appl	C 204	13	81.2	5176	3	US-09-610-040-6	Sequence 6, Appl
132	14	87.5	37601	4	US-09-949-016-15516	Sequence 15516, A	C 205	13	81.2	5176	3	US-10-267-761-6	Sequence 6, Appl
133	14	87.5	41613	4	US-09-949-016-16125	Sequence 16125, A	C 206	13	81.2	7210	4	US-09-634-238-15	Sequence 15, Appl
134	14	87.5	46984	4	US-09-949-016-15254	Sequence 15254, A	C 207	13	81.2	7736	3	US-09-949-016-15762	Sequence 15, Appl
C 135	14	87.5	107980	4	US-09-949-016-13765	Sequence 13765, A	C 208	13	81.2	10862	3	US-09-058-411-1	Sequence 1, Appl
C 136	14	87.5	162470	3	US-09-345-882-1	Sequence 1, Appl	C 209	13	81.2	10862	4	US-09-705-949-1	Sequence 1, Appl
C 137	14	87.5	209210	1	US-09-949-016-15094	Sequence 15094, A	C 210	13	81.2	10892	4	US-09-452-638-52	Sequence 52, Appl
C 138	13	81.2	16	1	US-08-281-106-50	Sequence 50, Appl	C 211	13	81.2	12566	3	US-08-961-527-149	Sequence 149, App
139	13	81.2	16	1	US-08-199-269-49	Sequence 49, Appl	C 212	13	81.2	14705	4	US-09-949-016-16249	Sequence 16249, App
140	13	81.2	16	1	US-08-199-269-50	Sequence 50, Appl	C 213	13	81.2	15995	4	US-09-949-016-16444	Sequence 16444, A
141	13	81.2	20	1	US-08-758-626-14	Sequence 14, Appl	C 214	13	81.2	24582	4	US-09-949-016-15482	Sequence 15482, A
142	13	81.2	20	1	PCT-US94-07684-14	Sequence 14, Appl	C 215	13	81.2	27490	4	US-09-902-540-1227	Sequence 1227, Ap
143	13	81.2	21	1	US-08-281-106-49	Sequence 49, Appl	C 216	13	81.2	33112	4	US-08-311-731A-121	Sequence 121, App
144	13	81.2	21	4	US-09-199-269-49	Sequence 49, Appl	C 217	13	81.2	35100	1	US-08-306-691B-19	Sequence 19, Appl
145	13	81.2	25	4	US-09-336-196G-80393	Sequence 80393, A	C 218	13	81.2	35100	5	PCT-US93-06251-19	Sequence 19, Appl
146	13	81.2	25	4	US-09-336-196G-80393	Sequence 80393, A	C 219	13	81.2	35603	4	US-09-949-016-11863	Sequence 11863, A
C 147	13	81.2	30	1	US-08-051-935A-45	Sequence 45, Appl	C 220	13	81.2	35604	4	US-09-949-016-12962	Sequence 12962, A
C 148	13	81.2	30	1	US-08-051-935A-46	Sequence 46, Appl	C 221	13	81.2	37115	4	US-09-949-016-13846	Sequence 13846, A
C 149	13	81.2	34	1	US-08-741-881-103	Sequence 103, App	C 222	13	81.2	48149	4	US-09-949-016-15258	Sequence 15258, A
C 150	13	81.2	34	1	US-08-739-158-103	Sequence 103, App	C 223	13	81.2	51336	4	US-09-949-016-16054	Sequence 16054, A
C 151	13	81.2	34	2	US-08-739-167-103	Sequence 103, App	C 224	13	81.2	52522	4	US-09-949-016-12150	Sequence 12150, A
C 152	13	81.2	34	3	US-08-404-796-103	Sequence 103, App	C 225	13	81.2	59252	4	US-09-949-016-15374	Sequence 15374, A
C 153	13	81.2	34	3	US-08-931-869-103	Sequence 103, App	C 226	13	81.2	68834	4	US-09-949-016-11959	Sequence 11959, A
C 154	13	81.2	34	3	US-08-483-511-8	Sequence 8, Appl	C 227	13	81.2	68834	4	US-09-949-016-11959	Sequence 11959, A
C 155	13	81.2	34	3	US-09-350-399-103	Sequence 103, App	C 228	13	81.2	79578	4	US-09-949-016-16336	Sequence 16336, A
C 156	13	81.2	34	3	US-09-336-140A-103	Sequence 103, App	C 229	13	81.2	84171	4	US-09-949-016-16336	Sequence 16336, A
C 157	13	81.2	34	5	PCT-US93-01009-8	Sequence 8, Appl	C 230	13	81.2	106929	4	US-09-949-016-12060	Sequence 12060, A
C 158	13	81.2	35	1	US-08-361-920-59	Sequence 59, Appl	C 231	13	81.2	106929	4	US-09-949-016-16618	Sequence 16618, A
C 159	13	81.2	35	1	US-08-479-939-59	Sequence 59, Appl	C 232	13	81.2	125188	4	US-09-949-016-11960	Sequence 11960, A
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C 163	13	81.2	308	4	US-09-107-433-173	Sequence 173, Ap	C 236	13	81.2	251769	4	US-09-949-016-13185	Sequence 13185, A
C 164	13	81.2	348	4	US-09-502-540-2036	Sequence 2036, Ap	C 237	13	81.2	251769	4	US-09-949-016-13186	Sequence 13186, A
C 165	13	81.2	444	4	US-09-270-767-27764	Sequence 27764, A	C 238	13	81.2	266748	4	US-09-949-016-13187	Sequence 13187, A
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C 173	13	81.2	601	4	US-09-949-016-160986	Sequence 160986, A	C 246	12	75.0	16	5	PCT-US96-10984-36	Sequence 36, Appl

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C 249	12	75.0	19	4	US-09-940-244-180	Sequence 180, App	C 322	12	75.0	601	4	US-09-949-016-32483	Sequence 32483, A
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C 251	12	75.0	20	4	US-09-940-244-188	Sequence 188, App	C 324	12	75.0	601	4	US-09-949-016-41367	Sequence 41367, A
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C 255	12	75.0	21	4	US-09-940-244-186	Sequence 186, App	C 328	12	75.0	601	4	US-09-949-016-47081	Sequence 47081, A
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C 258	12	75.0	28	4	US-09-940-244-170	Sequence 170, App	C 331	12	75.0	601	4	US-09-949-016-56983	Sequence 56983, A
C 259	12	75.0	28	4	US-09-940-244-175	Sequence 175, App	C 332	12	75.0	601	4	US-09-949-016-57908	Sequence 57908, A
C 260	12	75.0	28	4	US-09-940-244-185	Sequence 185, App	C 333	12	75.0	601	4	US-09-949-016-60943	Sequence 60943, A
C 261	12	75.0	30	3	US-08-691-563C-69	Sequence 69, App	C 334	12	75.0	601	4	US-09-949-016-60944	Sequence 60944, A
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C 263	12	75.0	30	4	US-08-979-847B-65	Sequence 65, App	C 336	12	75.0	601	4	US-09-949-016-63515	Sequence 63515, A
C 264	12	75.0	32	4	US-09-862-844-16	Sequence 16, App	C 337	12	75.0	601	4	US-09-949-016-63516	Sequence 63516, A
C 265	12	75.0	32	4	US-09-862-844-18	Sequence 18, App	C 338	12	75.0	601	4	US-09-949-016-63517	Sequence 63517, A
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C 267	12	75.0	41	4	US-09-940-244-183	Sequence 183, App	C 340	12	75.0	601	4	US-09-949-016-67802	Sequence 67802, A
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C 272	12	75.0	177	1	US-08-392-678-20	Sequence 20, App	C 345	12	75.0	601	4	US-09-949-016-116772	Sequence 116772, A
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C 276	12	75.0	240	4	US-09-248-796A-8192	Sequence 8192, App	C 349	12	75.0	601	4	US-09-949-016-137748	Sequence 137748, A
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C 281	12	75.0	344	4	US-09-513-599C-10821	Sequence 10821, A	C 354	12	75.0	601	4	US-09-949-016-153918	Sequence 153918, A
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C 283	12	75.0	386	4	US-09-270-767-2808	Sequence 2808, App	C 356	12	75.0	601	4	US-09-949-016-155999	Sequence 155999, A
C 284	12	75.0	386	4	US-09-270-767-18090	Sequence 18090, A	C 357	12	75.0	601	4	US-09-949-016-160000	Sequence 160000, A
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C 286	12	75.0	386	4	US-09-713-550-59	Sequence 59, App	C 359	12	75.0	601	4	US-09-949-016-165955	Sequence 165955, A
C 287	12	75.0	386	4	US-09-825-294-59	Sequence 59, App	C 360	12	75.0	601	4	US-09-949-016-167052	Sequence 167052, A
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C 294	12	75.0	429	4	US-08-979-847B-135	Sequence 135, App	C 367	12	75.0	601	4	US-09-949-016-175198	Sequence 175198, A
C 295	12	75.0	429	4	US-08-979-847B-136	Sequence 136, App	C 368	12	75.0	601	4	US-09-949-016-175209	Sequence 175209, A
C 296	12	75.0	429	4	US-08-979-847B-137	Sequence 137, App	C 369	12	75.0	601	4	US-09-949-016-175456	Sequence 175456, A
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C 299	12	75.0	438	4	US-08-979-847B-129	Sequence 129, App	C 372	12	75.0	601	4	US-09-949-016-187624	Sequence 187624, A
C 300	12	75.0	438	4	US-08-979-847B-130	Sequence 130, App	C 373	12	75.0	601	4	US-09-949-016-190556	Sequence 190556, A
C 301	12	75.0	438	4	US-08-979-847B-131	Sequence 131, App	C 374	12	75.0	601	4	US-09-949-016-192793	Sequence 192793, A
C 302	12	75.0	438	4	US-08-979-847B-201	Sequence 201, App	C 375	12	75.0	601	4	US-09-949-016-195071	Sequence 195071, A
C 303	12	75.0	441	4	US-09-248-796A-10012	Sequence 10012, A	C 376	12	75.0	601	4	US-09-949-016-199305	Sequence 199305, A
C 304	12	75.0	444	4	US-09-248-796A-1401	Sequence 1401, App	C 377	12	75.0	601	4	US-09-949-016-203890	Sequence 203890, A
C 305	12	75.0	453	4	US-09-909-595-13	Sequence 13, App	C 378	12	75.0	601	4	US-09-949-016-203394	Sequence 203394, A
C 306	12	75.0	466	4	US-09-270-767-10433	Sequence 10433, App	C 379	12	75.0	601	4	US-09-949-016-203395	Sequence 203395, A
C 307	12	75.0	500	4	US-09-270-767-5945	Sequence 5945, App	C 380	12	75.0	601	4	US-09-949-016-203396	Sequence 203396, A
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C 313	12	75.0	532	4	US-09-621-976-19174	Sequence 19174, A	C 386	12	75.0	601	4	US-08-470-006A-8	Sequence 8, App
C 314	12	75.0	553	4	US-09-270-767-14843	Sequence 14843, A	C 387	12	75.0	601	4	US-08-691-563C-8	Sequence 8, App
C 315	12	75.0	601	4	US-09-949-016-18481	Sequence 18481, A	C 388	12	75.0	601	4	US-09-300-990-8	Sequence 8, App
C 316	12	75.0	601	4	US-09-949-016-19001	Sequence 19001, A	C 389	12	75.0	601	4	US-09-133-411-8	Sequence 8, App
C 317	12	75.0	601	4	US-09-949-016-19001	Sequence 19001, A	C 390	12	75.0	601	4	US-09-374-766-8	Sequence 8, App
C 318	12	75.0	601	4	US-09-949-016-20068	Sequence 20068, A	C 391	12	75.0	601	4	US-08-979-847B-8	Sequence 8, App
C 319	12	75.0	601	4	US-09-949-016-20069	Sequence 20069, A	C 392	12	75.0	601	4	US-09-248-796A-707	Sequence 707, App

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394	12	75.0	741	2	US-08-471-969-9	Sequence 9, Appl1	467	12	75.0	1701	4	US-09-799-451-615	Sequence 615, App
395	12	75.0	741	2	US-08-384-137-9	Sequence 9, Appl1	468	12	75.0	1846	3	US-09-336-536-37	Sequence 37, Appl1
396	12	75.0	741	2	US-08-470-006A-9	Sequence 9, Appl1	469	12	75.0	1903	3	US-08-581-148C-15	Sequence 15, Appl1
397	12	75.0	741	3	US-08-691-563C-9	Sequence 9, Appl1	470	12	75.0	1931	4	US-09-429-906B-5	Sequence 5, Appl1
398	12	75.0	741	3	US-09-200-990-9	Sequence 9, Appl1	471	12	75.0	1934	4	US-09-451-938	Sequence 938, App
399	12	75.0	741	3	US-09-133-411-9	Sequence 9, Appl1	472	12	75.0	1958	3	US-09-215-221-9	Sequence 9, Appl1
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401	12	75.0	741	4	US-08-979-847B-9	Sequence 9, Appl1	474	12	75.0	1991	3	US-09-173-151A-19	Sequence 19, App
402	12	75.0	741	3	US-09-359-301A-32	Sequence 32, Appl1	475	12	75.0	2205	4	US-09-949-016-736	Sequence 736, App
403	12	75.0	767	3	US-08-858-207A-231	Sequence 38, Appl1	476	12	75.0	2295	4	US-09-270-767-12465	Sequence 12465, A
404	12	75.0	791	3	US-08-250-124A-38	Sequence 231, App	477	12	75.0	2304	2	US-08-548-159-6	Sequence 87, Appl1
405	12	75.0	804	4	US-09-583-110-1429	Sequence 624, App	478	12	75.0	2351	2	US-08-979-847B-88	Sequence 88, Appl1
406	12	75.0	816	4	US-09-540-236-624	Sequence 75, Appl1	479	12	75.0	2364	3	US-08-880-080-1	Sequence 1, Appl1
407	12	75.0	843	4	US-09-107-433-75	Sequence 5138, Ap	480	12	75.0	2373	3	US-08-691-563C-57	Sequence 57, Appl1
408	12	75.0	861	2	US-08-778-912A-1	Sequence 1, Appl1	481	12	75.0	2391	3	US-09-374-766-57	Sequence 57, Appl1
409	12	75.0	874	2	US-09-541-941B-2	Sequence 1099, Ap	482	12	75.0	2391	4	US-08-979-847B-53	Sequence 53, Appl1
410	12	75.0	875	4	US-08-976-594-1099	Sequence 6, Appl1	483	12	75.0	2400	6	5256558-6	Patent No. 5256558
411	12	75.0	876	2	US-08-778-912A-6	Sequence 330, App	484	12	75.0	2400	6	5256558-6	Patent No. 5256558
412	12	75.0	876	3	US-09-541-941B-6	Sequence 30732, A	485	12	75.0	2454	3	US-09-248-796A-935	Sequence 935, App
413	12	75.0	876	3	US-09-583-110-330	Sequence 797, App	486	12	75.0	2537	3	US-09-173-151A-34	Sequence 34, Appl1
414	12	75.0	900	4	US-09-270-767-30732	Sequence 30732, A	487	12	75.0	2617	3	US-09-724-864-10	Sequence 10, Appl1
415	12	75.0	901	4	US-09-107-433-797	Sequence 2100, Ap	488	12	75.0	2628	4	US-09-949-016-3889	Sequence 3889, Ap
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417	12	75.0	921	4	US-09-328-352-935	Sequence 2935, Ap	490	12	75.0	2754	1	US-08-760-936-1	Sequence 1, Appl1
418	12	75.0	927	4	US-09-671-317-266	Sequence 266, App	491	12	75.0	2754	2	US-09-225-02A-1	Sequence 1, Appl1
419	12	75.0	927	4	US-09-270-767-2537	Sequence 2537, Ap	492	12	75.0	2772	4	US-09-949-016-5532	Sequence 1, Appl1
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425	12	75.0	1044	4	US-09-270-767-28307	Sequence 1297, Ap	498	12	75.0	3079	4	US-09-970-966-184	Sequence 184, App
426	12	75.0	1075	4	US-09-016-434-1297	Sequence 14, Appl1	499	12	75.0	3079	4	US-09-640-173-184	Sequence 184, App
427	12	75.0	1111	4	US-09-227-357-14	Sequence 6907, Ap	500	12	75.0	3079	4	US-09-712-550-184	Sequence 184, App
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437	12	75.0	1158	3	US-09-374-766-1	Sequence 1, Appl1	510	12	75.0	3582	2	US-08-400-159-9	Sequence 9, Appl1
438	12	75.0	1158	4	US-09-374-766-1	Sequence 1, Appl1	511	12	75.0	3582	3	US-08-611-729A-9	Sequence 9, Appl1
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441	12	75.0	1203	4	US-09-374-766-1	Sequence 100, App	514	12	75.0	3672	2	US-08-390-888A-2	Sequence 2, Appl1
442	12	75.0	1203	4	US-09-374-766-1	Sequence 948, App	515	12	75.0	3754	4	US-09-361-709B-6	Sequence 6, Appl1
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444	12	75.0	1245	3	US-08-475-742-16	Sequence 1427, Ap	517	12	75.0	3999	4	US-09-640-173-177	Sequence 177, App
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446	12	75.0	1266	4	US-09-540-236-1437	Sequence 1427, Ap	519	12	75.0	3999	4	US-09-825-264-177	Sequence 177, App
447	12	75.0	1266	4	US-09-540-236-1437	Sequence 2377, Ap	520	12	75.0	3999	4	US-09-825-264-177	Sequence 177, App
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454	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	527	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
455	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	528	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
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457	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	530	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
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459	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	532	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
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461	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	534	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
462	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	535	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
463	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	536	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
464	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	537	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App
465	12	75.0	1386	4	US-09-352-991A-15065	Sequence 231, App	538	12	75.0	4308	4	US-09-799-451-156	Sequence 156, App

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603	12	75.0	23669	4	US-09-949-016-15266	Sequence 15266, A	676	12	75.0	62909	4	US-09-596-002-32	Sequence 32, Appl1
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609	12	75.0	23826	4	US-09-949-016-16715	Sequence 16715, A	682	12	75.0	67002	4	US-09-949-016-16803	Sequence 16803, A
610	12	75.0	24154	4	US-09-949-016-16374	Sequence 16374, A	683	12	75.0	70252	4	US-09-949-016-13375	Sequence 13375, A
611	12	75.0	24715	4	US-09-949-016-12979	Sequence 12979, A	684	12	75.0	70253	4	US-09-949-016-12748	Sequence 12748, A

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C 687	12	75.0	76962	4	US-09-949-016-17482	Sequence 17482, A	C 760	12	75.0	330830	4	US-09-949-016-14720	Sequence 14720, A
C 688	12	75.0	77772	4	US-09-949-016-17417	Sequence 17417, A	C 761	12	75.0	678533	4	US-09-949-016-14577	Sequence 14577, A
C 689	12	75.0	77997	4	US-09-949-016-12249	Sequence 12249, A	C 762	12	75.0	678533	4	US-09-949-016-14578	Sequence 14578, A
C 690	12	75.0	78125	4	US-09-949-016-16006	Sequence 16006, A	C 763	12	75.0	767677	4	US-09-949-016-12147	Sequence 12147, A
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C 695	12	75.0	81585	4	US-09-949-016-15427	Sequence 15427, A	C 768	12	75.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 696	12	75.0	81827	4	US-09-949-016-15623	Sequence 15623, A	C 769	12	75.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
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C 698	12	75.0	87752	4	US-09-949-016-16807	Sequence 16807, A	C 771	11	68.8	16	1	US-08-281-106-46	Sequence 46, Appl
C 699	12	75.0	92344	4	US-09-949-016-16802	Sequence 16802, A	C 772	11	68.8	16	1	US-09-199-269-46	Sequence 27, Appl
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C 701	12	75.0	94142	4	US-09-949-016-16553	Sequence 16553, A	C 774	11	68.8	19	4	PCT-US96-10984-27	Sequence 27, Appl
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C 704	12	75.0	96327	4	US-09-949-016-17235	Sequence 17235, A	C 777	11	68.8	19	6	5183745-11	Sequence 6183745, Ap
C 705	12	75.0	100463	4	US-09-949-016-16541	Sequence 16541, A	C 778	11	68.8	19	6	5183745-11	Sequence 6183745, Ap
C 706	12	75.0	100468	4	US-09-949-016-12511	Sequence 12511, A	C 779	11	68.8	20	2	US-08-501-968-17	Sequence 17, Appl
C 707	12	75.0	101300	4	US-09-949-016-13725	Sequence 13725, A	C 780	11	68.8	20	2	US-09-467-642-36	Sequence 36, Appl
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C 710	12	75.0	104077	4	US-09-949-016-13593	Sequence 13593, A	C 783	11	68.8	25	4	US-09-396-196G-16744	Sequence 16744, Ap
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C 713	12	75.0	107800	4	US-09-949-016-13118	Sequence 13118, A	C 786	11	68.8	25	4	US-09-396-196G-57071	Sequence 57071, A
C 714	12	75.0	107937	4	US-09-949-016-17192	Sequence 17192, A	C 787	11	68.8	25	4	US-09-396-196G-17767	Sequence 17767, A
C 715	12	75.0	116425	4	US-09-949-016-11809	Sequence 11809, A	C 788	11	68.8	25	4	US-09-396-196G-17768	Sequence 17768, A
C 716	12	75.0	116595	4	US-09-949-016-17565	Sequence 17565, A	C 789	11	68.8	25	4	US-09-396-196G-92204	Sequence 92204, A
C 717	12	75.0	117807	4	US-09-949-016-15525	Sequence 15525, A	C 790	11	68.8	25	4	US-09-396-196G-92204	Sequence 92204, A
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C 725	12	75.0	147840	4	US-09-949-016-12449	Sequence 12449, A	C 800	11	68.8	121	4	US-09-513-999C-30919	Sequence 30919, A
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C 727	12	75.0	153643	4	US-09-949-016-12147	Sequence 12147, A	C 802	11	68.8	160	4	US-09-513-999C-20547	Sequence 20547, A
C 728	12	75.0	156324	4	US-09-949-016-13749	Sequence 13749, A	C 803	11	68.8	162	2	US-08-890-979-22	Sequence 22, Appl
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C 732	12	75.0	177251	4	US-09-949-016-15841	Sequence 15841, A	C 807	11	68.8	181	4	US-09-513-999C-2581	Sequence 2581, Ap
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C 744	12	75.0	222452	4	US-09-949-016-12968	Sequence 12968, A	C 819	11	68.8	258	4	US-09-640-211A-1828	Sequence 1828, Ap
C 745	12	75.0	234884	4	US-09-949-016-16420	Sequence 16420, A	C 820	11	68.8	265	4	US-09-328-352-1126	Sequence 352, Ap
C 746	12	75.0	236474	4	US-09-949-016-13418	Sequence 13418, A	C 821	11	68.8	265	4	US-09-621-976-1570	Sequence 3570, Ap
C 747	12	75.0	239527	2	US-08-724-394A-21	Sequence 21, Appl	C 822	11	68.8	267	3	US-09-172-711-37	Sequence 37, Appl
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C 749	12	75.0	246240	2	US-08-724-394A-22	Sequence 22, Appl	C 824	11	68.8	277	4	US-09-313-294A-3324	Sequence 3324, Ap
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C 754	12	75.0	305481	4	US-09-949-016-17550	Sequence 17550, A	C 829	11	68.8	291	4	US-09-313-294A-1966	Sequence 1966, Ap
C 755	12	75.0	321022	4	US-09-949-016-11852	Sequence 11852, A	C 830	11	68.8	291	4	US-09-313-294A-1966	Sequence 1966, Ap
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C 834	11	68.8	300	4	US-08-781-986A-2021	Sequence 2021, Ap	C 907	11	68.8	435	3	US-09-032-894-96	Sequence 96, Appl
C 835	11	68.8	309	4	US-09-540-236-1567	Sequence 1567, Ap	C 908	11	68.8	435	3	US-09-031-626-7	Sequence 7, Appl
C 836	11	68.8	309	4	US-09-248-796A-656	Sequence 656, App	C 909	11	68.8	435	3	US-09-031-626-96	Sequence 96, Appl
C 837	11	68.8	312	4	US-09-513-999C-879	Sequence 879, App	C 910	11	68.8	435	4	US-09-621-976-3558	Sequence 358, Ap
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C 839	11	68.8	324	4	US-09-248-796A-8591	Sequence 8591, Ap	C 912	11	68.8	435	4	US-09-270-767-8285	Sequence 2885, Ap
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C 841	11	68.8	329	4	US-09-621-976-71	Sequence 71, Appl	C 914	11	68.8	500	4	US-09-270-767-23567	Sequence 23567, A
C 842	11	68.8	332	4	US-09-513-999C-21292	Sequence 21292, A	C 915	11	68.8	501	4	US-09-621-976-1522	Sequence 1522, Ap
C 843	11	68.8	335	4	US-09-621-976-14610	Sequence 14610, A	C 916	11	68.8	502	4	US-09-513-999C-11313	Sequence 13133, A
C 844	11	68.8	342	4	US-09-489-039A-5145	Sequence 5145, Ap	C 917	11	68.8	505	4	US-09-621-976-16639	Sequence 16439, A
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C 846	11	68.8	348	4	US-09-270-767-2398	Sequence 2398, Ap	C 919	11	68.8	519	4	US-09-949-016-89378	Sequence 89378, A
C 847	11	68.8	348	4	US-09-270-767-17680	Sequence 17680, A	C 920	11	68.8	523	4	US-09-621-976-16684	Sequence 16684, Ap
C 848	11	68.8	348	4	US-09-513-999C-338	Sequence 338, App	C 921	11	68.8	534	3	US-09-370-807-15	Sequence 15, Appl
C 849	11	68.8	349	4	US-09-270-767-65482	Sequence 26482, A	C 922	11	68.8	534	3	US-09-921-259-15	Sequence 15, Appl
C 850	11	68.8	352	4	US-09-621-976-17996	Sequence 17996, A	C 923	11	68.8	542	4	US-09-621-976-275	Sequence 275, Appl
C 851	11	68.8	353	4	US-09-621-976-16151	Sequence 16151, A	C 924	11	68.8	551	4	US-09-647-224A-21	Sequence 21, Appl
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C 853	11	68.8	359	4	US-09-338-933-66	Sequence 66, Appl	C 926	11	68.8	571	3	US-09-312-283C-352	Sequence 352, App
C 854	11	68.8	359	4	US-09-215-681-66	Sequence 66, Appl	C 927	11	68.8	575	3	US-09-385-283C-473	Sequence 473, App
C 855	11	68.8	359	4	US-09-667-857-66	Sequence 66, Appl	C 928	11	68.8	587	3	US-09-026-601-39	Sequence 39, Appl
C 856	11	68.8	363	4	US-09-513-999C-1733	Sequence 1733, Appl	C 929	11	68.8	587	4	US-09-702-705-1753	Sequence 1753, App
C 857	11	68.8	372	3	US-09-221-0178-317	Sequence 317, App	C 930	11	68.8	587	4	US-09-736-457-1753	Sequence 1753, Ap
C 858	11	68.8	375	4	US-09-107-433-1237	Sequence 1237, App	C 931	11	68.8	587	4	US-09-671-325-1753	Sequence 1753, Ap
C 859	11	68.8	375	4	US-09-270-767-706	Sequence 706, App	C 932	11	68.8	587	4	US-09-658-824-1753	Sequence 1753, Ap
C 860	11	68.8	382	4	US-09-270-767-15988	Sequence 15988, A	C 933	11	68.8	587	4	US-09-621-976-1526	Sequence 1526, Ap
C 861	11	68.8	382	4	US-09-513-999C-927	Sequence 927, App	C 934	11	68.8	591	3	US-09-404-879A-56	Sequence 56, Appl
C 862	11	68.8	386	4	US-09-513-999C-3075	Sequence 3075, Ap	C 935	11	68.8	591	4	US-09-338-933-56	Sequence 56, Appl
C 863	11	68.8	390	4	US-09-513-999C-225	Sequence 225, App	C 936	11	68.8	591	4	US-09-215-681-56	Sequence 56, Appl
C 864	11	68.8	397	4	US-09-513-999C-3856	Sequence 3856, App	C 937	11	68.8	591	4	US-09-215-681-56	Sequence 56, Appl
C 865	11	68.8	401	4	US-09-465-529-77	Sequence 77, Appl	C 938	11	68.8	593	4	US-09-667-857-56	Sequence 56, Appl
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C 867	11	68.8	414	4	US-09-328-111-478	Sequence 478, App	C 940	11	68.8	595	4	US-09-270-767-78	Sequence 78, Appl
C 868	11	68.8	419	3	US-09-702-705-573	Sequence 573, App	C 941	11	68.8	595	4	US-09-949-016-15360	Sequence 15360, A
C 869	11	68.8	423	4	US-09-736-457-573	Sequence 573, App	C 942	11	68.8	601	4	US-09-949-016-16333	Sequence 16333, A
C 870	11	68.8	423	4	US-09-614-124B-573	Sequence 573, App	C 943	11	68.8	601	4	US-09-949-016-16310	Sequence 16310, A
C 871	11	68.8	423	4	US-09-611-325-573	Sequence 573, App	C 944	11	68.8	601	4	US-09-949-016-19466	Sequence 19466, A
C 872	11	68.8	423	4	US-09-589-184-573	Sequence 573, App	C 945	11	68.8	601	4	US-09-949-016-21407	Sequence 21407, A
C 873	11	68.8	423	4	US-09-658-824-573	Sequence 573, App	C 946	11	68.8	601	4	US-09-949-016-21408	Sequence 21408, A
C 874	11	68.8	425	4	US-09-513-999C-3857	Sequence 3857, App	C 947	11	68.8	601	4	US-09-949-016-21409	Sequence 21409, A
C 875	11	68.8	429	4	US-09-513-999C-8354	Sequence 8354, Ap	C 948	11	68.8	601	4	US-09-949-016-23280	Sequence 23280, A
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C 877	11	68.8	441	4	US-09-270-767-6479	Sequence 6479, Ap	C 950	11	68.8	601	4	US-09-949-016-24886	Sequence 24886, A
C 878	11	68.8	441	4	US-09-270-767-6479	Sequence 6479, Ap	C 951	11	68.8	601	4	US-09-949-016-25387	Sequence 25387, A
C 879	11	68.8	441	4	US-09-621-976-1761	Sequence 1761, A	C 952	11	68.8	601	4	US-09-949-016-26333	Sequence 26333, A
C 880	11	68.8	446	3	US-08-998-416-195	Sequence 195, App	C 953	11	68.8	601	4	US-09-949-016-26562	Sequence 26562, A
C 881	11	68.8	446	3	US-09-621-976-13235	Sequence 13235, A	C 954	11	68.8	601	4	US-09-949-016-26599	Sequence 26599, A
C 882	11	68.8	448	4	US-09-270-767-5655	Sequence 5655, Ap	C 955	11	68.8	601	4	US-09-949-016-27173	Sequence 27173, A
C 883	11	68.8	448	4	US-09-902-540-1640	Sequence 1640, Ap	C 956	11	68.8	601	4	US-09-949-016-27438	Sequence 27438, A
C 884	11	68.8	450	4	US-09-621-976-14151	Sequence 14151, A	C 957	11	68.8	601	4	US-09-949-016-28279	Sequence 28279, A
C 885	11	68.8	454	4	US-09-270-767-4284	Sequence 4284, Ap	C 958	11	68.8	601	4	US-09-949-016-28280	Sequence 28280, A
C 886	11	68.8	460	4	US-09-270-767-19566	Sequence 19566, A	C 959	11	68.8	601	4	US-09-949-016-28281	Sequence 28281, A
C 887	11	68.8	465	4	US-09-513-999C-32603	Sequence 32603, A	C 960	11	68.8	601	4	US-09-949-016-28282	Sequence 28282, A
C 888	11	68.8	471	3	US-09-328-111-439	Sequence 439, App	C 961	11	68.8	601	4	US-09-949-016-29009	Sequence 29009, A
C 889	11	68.8	471	3	US-09-248-796A-4073	Sequence 4073, Ap	C 962	11	68.8	601	4	US-09-949-016-30292	Sequence 30292, A
C 890	11	68.8	474	4	US-09-540-236-1158	Sequence 1158, Ap	C 963	11	68.8	601	4	US-09-949-016-31675	Sequence 31675, A
C 891	11	68.8	476	4	US-09-513-999C-13134	Sequence 13134, A	C 964	11	68.8	601	4	US-09-949-016-33127	Sequence 33127, A
C 892	11	68.8	477	4	US-09-513-999C-10326	Sequence 10326, A	C 965	11	68.8	601	4	US-09-949-016-33125	Sequence 33325, A
C 893	11	68.8	479	4	US-09-513-999C-8858	Sequence 8858, Ap	C 966	11	68.8	601	4	US-09-949-016-33324	Sequence 33324, A
C 894	11	68.8	479	4	US-09-471-276-770	Sequence 770, App	C 967	11	68.8	601	4	US-09-949-016-33325	Sequence 33325, A
C 895	11	68.8	482	4	US-09-621-976-16330	Sequence 16330, A	C 968	11	68.8	601	4	US-09-949-016-33326	Sequence 33326, A
C 896	11	68.8	482	4	US-09-513-999C-26168	Sequence 26168, A	C 969	11	68.8	601	4	US-09-949-016-33327	Sequence 33327, A
C 897	11	68.8	483	4	US-09-513-999C-32457	Sequence 32457, A	C 970	11	68.8	601	4		
C 898	11	68.8	483	4	US-09-621-976-2259	Sequence 2259, Ap	C 971	11	68.8	601	4		
C 899	11	68.8	485	4	US-08-600-430-3	Sequence 3, Appl	C 972	11	68.8	601	4		
C 900	11	68.8	492	3	US-09-270-767-9537	Sequence 9537, Ap	C 973	11	68.8	601	4		
C 901	11	68.8	494	4	US-09-270-767-9537	Sequence 9537, Ap	C 974	11	68.8	601	4		
C 902	11	68.8	494	4	US-09-270-767-9537	Sequence 9537, Ap	C 975	11	68.8	601	4		
C 903	11	68.8	494	4	US-09-270-767-9537	Sequence 9537, Ap	C 976	11	68.8	601	4		

C 977 11 68.8 601 4 US-09-949-016-33328 Sequence 33328, A
978 11 68.8 601 4 US-09-949-016-35476 Sequence 35476, A
979 11 68.8 601 4 US-09-949-016-35477 Sequence 35477, A
980 11 68.8 601 4 US-09-949-016-35478 Sequence 35478, A
981 11 68.8 601 4 US-09-949-016-35559 Sequence 35559, A
982 11 68.8 601 4 US-09-949-016-36379 Sequence 36379, A
983 11 68.8 601 4 US-09-949-016-36398 Sequence 36398, A
984 11 68.8 601 4 US-09-949-016-37986 Sequence 37986, A
985 11 68.8 601 4 US-09-949-016-38250 Sequence 38250, A
986 11 68.8 601 4 US-09-949-016-38251 Sequence 38251, A
987 11 68.8 601 4 US-09-949-016-38252 Sequence 38252, A
988 11 68.8 601 4 US-09-949-016-38487 Sequence 38487, A
989 11 68.8 601 4 US-09-949-016-38500 Sequence 38500, A
990 11 68.8 601 4 US-09-949-016-39557 Sequence 39557, A
991 11 68.8 601 4 US-09-949-016-41564 Sequence 41564, A
992 11 68.8 601 4 US-09-949-016-43078 Sequence 43078, A
993 11 68.8 601 4 US-09-949-016-43207 Sequence 43207, A
994 11 68.8 601 4 US-09-949-016-43436 Sequence 43436, A
995 11 68.8 601 4 US-09-949-016-43665 Sequence 43665, A
996 11 68.8 601 4 US-09-949-016-44712 Sequence 44712, A
997 11 68.8 601 4 US-09-949-016-44713 Sequence 44713, A
998 11 68.8 601 4 US-09-949-016-44999 Sequence 44999, A
999 11 68.8 601 4 US-09-949-016-46329 Sequence 46329, A
C1000 11 68.8 601 4 US-09-949-016-46407 Sequence 46407, A

ALIGNMENTS

RESULT 1
US-08-281-106-48
Sequence 48, Application US/08281106
Patent No. 5646262
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Antisense Oligonucleotides Against
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,106
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-281-106-48

Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCACCACCAAGCA 16
Db 1 AAAGCACCACCAAGCA 16

RESULT 2
US-09-199-269-48
Sequence 48, Application US/09199269
Patent No. 6503533
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Antisense Oligonucleotides Against
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,269
FILING DATE: 25-No. 6503533-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/281,106
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-199-269-48

Query Match 100.0%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCACCACCAAGCA 16
Db 1 AAAGCACCACCAAGCA 16

RESULT 3
US-09-155-885A-41
Sequence 41, Application US/09155885A
Patent No. 6709812
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-OCT-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-155-885A-41
Query Match 100.0%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16
RESULT 4
US-08-480-220A-22
Sequence 22, Application US/08480220A
Patent No. 5667974
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushahwar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla B.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770:US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' phosphate
LOCATION: 1
FEATURE:
NAME/KEY: 3' fluorescein
LOCATION: 18
US-08-480-220A-22
Query Match 100.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16
RESULT 5
US-08-864-404-22
Sequence 22, Application US/08864404
Patent No. 5955598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushahwar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla B.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770:US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' phosphate
LOCATION: 1
FEATURE:
NAME/KEY: 3' fluorescein
LOCATION: 18
US-08-864-404-22

Query Match 100.0%; Score 16; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCAAGCA 16
Db 1 AAAGCCACCAAGCA 16

RESULT 6
US-09-155-885A-49

Sequence 49, Application US/09155885A
Patent No. 6709812

GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN

MAERTENS, RUDI

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

NUMBER OF SEQUENCES: 313

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A

FILING DATE: 08-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002

FILING DATE: 21-APR-1997

APPLICATION NUMBER: EP 96870053.4

FILING DATE: 19-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 2551-5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-155-885A-49

Query Match 100.0%; Score 16; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAGCCACCAAGCA 16
Db 1 AAAGCCACCAAGCA 16

RESULT 7

US-08-480-220A-21/c

Sequence 21, Application US/08480220A

Patent No. 5667974

GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry

APPLICANT: Mushahwar, Isa K.

TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/Abpd

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: Illinois

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A

FILING DATE: 07 JUN 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Potembek, Patricia E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5770.US.01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365

TELEFAX: 708/938-2623

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-480-220A-21

Query Match 100.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCAAGCA 16
Db 18 AAAGCCACCAAGCA 3

RESULT 8

US-08-480-220A-25/c

Sequence 25, Application US/08480220A

Patent No. 5667974

GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry

APPLICANT: Mushahwar, Isa K.

TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories D377/APeD
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-480-220A-25

Query Match 100.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3
DB

RESULT 9
US-08-864-404-21/C
Sequence 21, Application US/08864404
Patent No. 595598
GENERAL INFORMATION:
APPLICANT: Birkmeyer, Larry
APPLICANT: Mushawar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/APeD
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-35008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-864-404-21

Query Match 100.0%; Score 16; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3
DB

RESULT 10
US-08-864-404-25/C
Sequence 25, Application US/08864404
Patent No. 595598
GENERAL INFORMATION:
APPLICANT: Birkmeyer, Larry
APPLICANT: Mushawar, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/APeD
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-35008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA

FEATURE:
NAME/KEY: 5' fluorescein
LOCATION: 1
US-08-864-404-25

Query Match 100.0%; Score 16; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 18 AAAGCCACCCAGGCA 3

RESULT 11
US-08-501-968-18
Sequence 18, Application US/08501968
Patent No. 5985662
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Coweart
TITLE OF INVENTION: Antisense inhibition of Hepatitis B
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,968
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-501-968-18

Query Match 100.0%; Score 16; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 12
PCT-US96-10984-18
Sequence 18, Application PC/TUS9610984
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Coweart
TITLE OF INVENTION: Antisense inhibition of Hepatitis B
TITLE OF INVENTION: Virus Replication

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10984
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-10984-18

Query Match 100.0%; Score 16; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 13
US-08-281-106-45
Sequence 45, Application US/08281106
Patent No. 5646262
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
TITLE OF INVENTION: Antisense Oligonucleotides Against
TITLE OF INVENTION: Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,106
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 66683/112/SEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-281-106-45

Query Match 100.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 1 AAAGCCACCCAGGCA 16

RESULT 14
US-08-281-106-47
Sequence 47, Application US/08281106
Patent No. 5646262
GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
ATTORNEY/AGENT INFORMATION:
NAME: GERIN, John L.
TITLE OF INVENTION: Antisense Oligonucleotides Against
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,106
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/SEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-281-106-47

Query Match 100.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 6 AAAGCCACCCAGGCA 21

RESULT 15
US-08-287-337A-5
Sequence 5, Application US/08287337A
Patent No. 5728518
GENERAL INFORMATION:
APPLICANT: Ellen Carmichael
TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,337A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConci, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: TTI-109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-287-337A-5

Query Match 100.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 6 AAAGCCACCCAGGCA 21

RESULT 16
US-08-501-968-7
Sequence 7, Application US/08501968
Patent No. 5985662
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Cowser
TITLE OF INVENTION: Antisense Inhibition of Hepatitis B
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,968
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-501-968-7

Query Match 100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 3 AAAGCCACCCAGGCA 18

RESULT 17
US-09-199-269-45
Sequence 45, Application US/09199269
Patent No. 6503533

GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
GERIN, John L.

TITLE OF INVENTION: Antisense Oligonucleotides Against
Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,269
FILING DATE: 25-No. 6503533-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/281,106
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-199-269-45

Query Match 100.0%; Score 16; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 1 AAAGCCACCCAGGCA 16

RESULT 18
US-09-199-269-47
Sequence 47, Application US/09199269
Patent No. 6503533

GENERAL INFORMATION:
APPLICANT: KORBA, Brent E.
GERIN, John L.

TITLE OF INVENTION: Antisense Oligonucleotides Against
Hepatitis B Viral Replication
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,269
FILING DATE: 25-No. 6503533-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/281,106
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 66683/112/GEUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-199-269-47

Query Match 100.0%; Score 16; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 6 AAAGCCACCCAGGCA 21

RESULT 19
PCT-US95-00508-5
Sequence 5, Application PC/TUS9500508

GENERAL INFORMATION:
APPLICANT: Targetech, Inc.
TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00508
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/181,557
FILING DATE: January 12, 1994
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/287,337
FILING DATE: August 8, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: TTI-109CPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-00508-5

Query Match 100.0%; Score 16; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 6 AAAGCCACCCAGGCA 21

RESULT 20
PCT-US96-10984-7
GENERAL INFORMATION:
APPLICANT: Kevin Anderson and Lex Cowbert
TITLE OF INVENTION: Antisense Inhibition of Hepatitis B
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10984
FILING DATE: herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-10984-7

Query Match 100.0%; Score 16; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 3 AAAGCCACCCAGGCA 18

RESULT 21
US-08-758-626-13/c
Sequence 13, Application US/08758626
Patent No. 5736334
GENERAL INFORMATION:
APPLICANT: Uwe Spies
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,626
FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/422,018
FILING DATE:
APPLICATION NUMBER: 08/090,755
FILING DATE: JULY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainerd
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284, US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-938-2623
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-758-626-13

Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAAGCA 16
DB 23 AAAGCCACCAAGCA 8

RESULT 22
PCT-US94-07684-13/c
Sequence 13, Application US/
GENERAL INFORMATION:

APPLICANT: ABBOTT LABORATORIES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,755
FILING DATE: JULY 13, 1993
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
PCT-US94-07684-13

Query Match 100.0%; Score 16; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAAGCA 16
DB 23 AAAGCCACCAAGCA 8

RESULT 23
US-08-480-220A-19/c
Sequence 19, Application US/08480220A
Patent No. 5667974

GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushawat, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-480-220A-19

Query Match 100.0%; Score 16; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCAAGCA 16
DB 18 AAAGCCACCAAGCA 3

RESULT 24
US-08-480-220A-20/c
Sequence 20, Application US/08480220A
Patent No. 5667974

GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
APPLICANT: Mushawat, Isa K.
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,220A
FILING DATE: 07 JUN 1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-480-220A-20

Query Match 100.0%; Score 16; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3

RESULT 25
US-08-864-404-19/c
Sequence 19, Application US/08864404
Patent No. 5955598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3508
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-864-404-19

Query Match 100.0%; Score 16; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3

Db 18 AAAGCCACCCAGGCA 3

RESULT 26
US-08-864-404-20/c
Sequence 20, Application US/08864404
Patent No. 5955598
GENERAL INFORMATION:
APPLICANT: Birkenmeyer, Larry
TITLE OF INVENTION: METHOD FOR DETECTING NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE USING COMPETITIVE AMPLIFICATION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3508
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,404
FILING DATE: 28-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,220
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5770.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-6365
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-864-404-20

Query Match 100.0%; Score 16; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
18 AAAGCCACCCAGGCA 3

RESULT 27
US-08-758-626-25/c
Sequence 25, Application US/08758626
Patent No. 5736334
GENERAL INFORMATION:
APPLICANT: Uwe Spies
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,626
FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/422,018
FILING DATE:
APPLICATION NUMBER: 08/090,755
FILING DATE: JULY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Bralnard
REGISTRATION NUMBER: 32,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 50
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-758-626-25

Query Match 100.0%; Score 16; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAGCCACCCAGGCA 16
Db 23 AAAGCCACCCAGGCA 8

RESULT 28
PCT-US94-07684-25/c
Sequence 25, Application US/
GENERAL INFORMATION:
APPLICANT: ABBOTT LABORATORIES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
NUMBER OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,755
FILING DATE: JULY 13, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Bralnard
REGISTRATION NUMBER: 32,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 50
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
PCT-US94-07684-25

Query Match 100.0%; Score 16; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAGCCACCCAGGCA 16
Db 23 AAAGCCACCCAGGCA 8

RESULT 29
US-08-890-735C-3/c
Sequence 3, Application US/08890735C
Patent No. 6518014
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HEPADNAVIRUS CORES
FILE REFERENCE: DC44A
CURRENT APPLICATION NUMBER: US/08/890,735C
CURRENT FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 61
TYPE: DNA
ORGANISM: Hepatitis B Virus
US-08-890-735C-3

Query Match 100.0%; Score 16; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAGCCACCCAGGCA 16
Db 49 AAAGCCACCCAGGCA 34

RESULT 30
US-08-098-313-10/c
Sequence 10, Application US/08098313
Patent No. 5532124
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University and
TITLE OF INVENTION: Timothy Block and Robert Grafstrom
NUMBER OF INVENTION: Genetically Engineered Bacteria To
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESS: Mackiewicz & No. 5532124r18
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/098,313
FILING DATE: October 6, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 654,064 and PCT/US91/07294
FILING DATE: February 11, 1991 and October 4, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsall
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-0638
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 69
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: no
US-08-098-313-10

Query Match 100.0%; Score 16; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 55 AAAGCCACCCAGGCA 40

RESULT 31

PCT-US92-01188-10/C
Sequence 10, Application PC/TUS9201188
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University and
APPLICANT: Timothy Block and Robert Grafstrom
TITLE OF INVENTION: Genetically Engineered Bacteria To
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSER: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01188
FILING DATE: 19910211
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 654,064 and PCT/US91/07294
FILING DATE: February 11, 1991 and October 4, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 69
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: no
PCT-US92-01188-10

Query Match 100.0%; Score 16; DB 5; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 55 AAAGCCACCCAGGCA 40

RESULT 32

US-08-697-404-12/C
Sequence 12, Application US/08697404
Patent No. 5858732
GENERAL INFORMATION:
APPLICANT: N. A. Solomon
APPLICANT: S. R. Bouma
TITLE OF INVENTION: WIDE DYNAMIC RANGE NUCLEIC ACID
TITLE OF INVENTION: DETECTION USING AN AGGREGATE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,404
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,615A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yasser
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 5692, US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-2341
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA (HBV)
US-08-697-404-12

Query Match 100.0%; Score 16; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 33 AAAGCCACCCAGGCA 18

RESULT 33

US-08-287-337A-9/C
Sequence 9, Application US/08287337A
Patent No. 5728518
GENERAL INFORMATION:
APPLICANT: Ellen Carmichael
TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510

Query Match 100.0%; Score 16; DB 5; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,337A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: TTI-109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-287-337A-9

Query Match 100.0%; Score 16; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 49 AAAGCCACCCAGGCA 34

RESULT 34
US-08-075-520A-8/C
Sequence 8, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
ADDRESSEE: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460

FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-8

Query Match 100.0%; Score 16; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 25 AAAGCCACCCAGGCA 10

RESULT 35
US-08-075-520A-11/C
Sequence 11, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
ADDRESSEE: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-11

Query Match 100.0%; Score 16; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 25 AAAGCCACCCAGGCA 10

RESULT 36

US-08-075-520A-16/c

; Sequence 16, Application US/08075520A
; Patent No. 6020167
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans
; TITLE OF INVENTION: A Composition Used as a
; TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas Popovich
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible Compaq Prolinea 4/66
; OPERATING SYSTEM: MS-DOS Version 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,520A
; FILING DATE: January 31, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124775
; FILING DATE: December 19, 1990
; APPLICATION NUMBER: PCT/EP91/02460
; FILING DATE: December 19, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-075-520A-16

Query Match 100.0%; Score 16; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 25 AAAGCCACCCAGGCA 10

RESULT 37

US-08-445-585-2/c

; Sequence 2, Application US/08445585
; Patent No. 6277631
; GENERAL INFORMATION:
; APPLICANT: No. 6277631h, Michael
; APPLICANT: Broeker, Michael
; TITLE OF INVENTION: Recombinant Proteins with the
; TITLE OF INVENTION: Immunoreactivity of Hepatitis B Virus B Antigen (HBeAg), A

; TITLE OF INVENTION: Process for the Preparation Thereof and the Use Thereof In
; TITLE OF INVENTION: Immunoassays and Vaccines
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,585
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/846,194
; FILING DATE: 06-MAR-1992
; APPLICATION NUMBER: DE P 41 07 612.5
; FILING DATE: 03-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: P-36,228
; REFERENCE/DOCKET NUMBER: 02481.1162-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..477
; US-08-445-585-2

Query Match 100.0%; Score 16; DB 3; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 25 AAAGCCACCCAGGCA 10

RESULT 38

US-08-075-520A-4/c

; Sequence 4, Application US/08075520A
; Patent No. 6020167
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans
; TITLE OF INVENTION: A Composition Used as a
; TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas Popovich
; ADDRESSEE: & Associates
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage

```
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-4

Query Match      100.0%; Score 16; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
        |||||
        25 AAAGCCACCCCAAGCA 10

RESULT 39
US-08-075-520A-5/c
Sequence 5, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Thomas E. Popovich, Thomas Popovich
ADDRESSEE: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-5

Query Match      100.0%; Score 16; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
        |||||
        25 AAAGCCACCCCAAGCA 10

RESULT 40
US-08-075-520A-35/c
Sequence 35, Application US/08075520A
Patent No. 6020167
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Thomas E. Popovich, Thomas Popovich
ADDRESSEE: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-075-520A-35

Query Match      100.0%; Score 16; DB 3; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
        |||||
        25 AAAGCCACCCCAAGCA 10
```

Fri Apr 1 07:57:26 2005

us-09-888-164-29.oligo.rml

Page 23

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Job time : 120 secs

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:05:42 ; Search time 276 Seconds
(without alignments)
350.869 Million cell updates/sec

Title: US-09-888-164-29

Perfect score: 16
Sequence: 1 aaagcaccacgaagca 16

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 5607317 seqs, 302624599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA:*

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3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/prodata/1/pubpna/PC7US_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	16	100.0	17	10	US-09-877-478-2378
5	16	100.0	17	17	US-10-342-902-1755
6	16	100.0	17	17	US-10-342-902-2378
7	16	100.0	17	18	US-10-669-841-1755
8	16	100.0	17	18	US-10-669-841-2181
9	16	100.0	18	17	US-10-453-792-49
10	16	100.0	19	17	US-10-244-647-54
11	16	100.0	19	17	US-10-244-647-574

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C 13	16	100.0	19	17	US-10-244-647-577	Sequence 577, App
C 14	16	100.0	19	17	US-10-244-647-700	Sequence 700, App
C 15	16	100.0	19	17	US-10-244-647-1220	Sequence 1220, App
C 16	16	100.0	19	17	US-10-244-647-1222	Sequence 1222, App
C 17	16	100.0	19	17	US-10-244-647-1223	Sequence 1223, App
C 18	16	100.0	23	17	US-10-244-647-1296	Sequence 1296, App
C 19	16	100.0	54	9	US-09-756-500-4	Sequence 4, Appl
C 20	16	100.0	114	17	US-10-394-896-8	Sequence 8, Appl
C 21	16	100.0	291	17	US-10-394-896-11	Sequence 11, Appl
C 22	16	100.0	390	17	US-10-394-896-16	Sequence 16, Appl
C 23	16	100.0	534	17	US-10-394-896-4	Sequence 4, Appl
C 24	16	100.0	534	17	US-10-394-896-5	Sequence 5, Appl
C 25	16	100.0	560	19	US-10-478-633A-69	Sequence 69, Appl
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C 74	16	100.0	3221	17	US-10-453-792-279	Sequence 279, Appl
C 75	16	100.0	3221	17	US-10-453-792-281	Sequence 281, Appl
C 76	16	100.0	3221	17	US-10-453-792-282	Sequence 282, Appl
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C 82	16	100.0	5077	17	US-10-464-366-103	Sequence 103, Appl
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C 96	15	93.8	394	18	US-10-425-115-29773	Sequence 29773, A	169	14	87.5	609	13	US-10-027-633-184552	Sequence 184552,
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C 104	15	93.8	864	15	US-10-128-714-2456	Sequence 2456, Ap	177	14	87.5	831	17	US-10-424-599-138926	Sequence 138926,
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C 123	14	87.5	17	10	US-09-877-478-2379	Sequence 2379, Ap	196	14	87.5	3454	17	US-10-703-864-48	Sequence 48, Appl
C 124	14	87.5	17	17	US-10-342-902-418	Sequence 2379, Ap	197	14	87.5	3523	17	US-10-264-049-490	Sequence 490, Ap
C 125	14	87.5	17	17	US-10-342-902-2379	Sequence 2379, Ap	198	14	87.5	3522	14	US-10-116-802-133	Sequence 133, Ap
C 126	14	87.5	17	18	US-10-669-841-418	Sequence 418, Ap	199	14	87.5	3535	14	US-10-238-876-1	Sequence 1, Appl
C 127	14	87.5	17	18	US-10-669-841-2182	Sequence 2182, Ap	200	14	87.5	3535	15	US-10-177-293-1	Sequence 1, Appl
C 128	14	87.5	19	17	US-10-669-841-2182	Sequence 61, Appl	201	14	87.5	3535	17	US-10-159-553-88	Sequence 288, Ap
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C 130	14	87.5	21	17	US-10-244-647-1340	Sequence 1340, Ap	203	14	87.5	3535	18	US-10-775-920-195	Sequence 195, Ap
C 131	14	87.5	21	17	US-10-244-647-1340	Sequence 1344, Ap	204	14	87.5	3535	18	US-10-473-974-128	Sequence 128, Ap
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C 133	14	87.5	21	18	US-10-444-853A-183	Sequence 183, Appl	206	14	87.5	4236	17	US-10-282-122A-26916	Sequence 26916, A
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C 136	14	87.5	21	19	US-10-826-966-179	Sequence 179, Appl	209	14	87.5	6599	10	US-09-952-213D-4	Sequence 4, Appl
C 137	14	87.5	21	19	US-10-826-966-183	Sequence 183, Appl	210	14	87.5	1661	10	US-09-957-956-8	Sequence 8, Appl
C 138	14	87.5	25	19	US-10-719-900-402113	Sequence 402113,	211	14	87.5	29921	18	US-10-719-993-6848	Sequence 6848, Ap
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C 140	14	87.5	49	16	US-10-080-299-39	Sequence 39, Appl	213	14	87.5	43229	13	US-10-087-192-517	Sequence 517, Appl
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C 148	14	87.5	352	17	US-10-424-599-47963	Sequence 47963, A	221	13	81.2	17	10	US-09-877-478-1150	Sequence 1150, Ap
C 149	14	87.5	355	9	US-09-880-107-2955	Sequence 2955, Ap	222	13	81.2	17	10	US-09-877-478-1756	Sequence 1756, Ap
C 150	14	87.5	395	9	US-09-998-598-825	Sequence 825, Appl	223	13	81.2	17	17	US-10-342-902-1150	Sequence 1150, Ap
C 151	14	87.5	412	18	US-10-425-115-166783	Sequence 166783,	224	13	81.2	17	17	US-10-342-902-1150	Sequence 1150, Ap
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C 156	14	87.5	467	9	US-09-770-444-279	Sequence 58046, A	229	13	81.2	21	17	US-10-244-647-1371	Sequence 1371, Ap
C 157	14	87.5	499	18	US-10-425-115-58046	Sequence 58046, A	230	13	81.2	21	17	US-10-244-647-1415	Sequence 1415, Ap

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C 242	13	81.2	163	17	US-10-424-599-34732	Sequence 34732, A	C 315	13	81.2	604	13	US-10-027-632-309950	Sequence 309950, A
C 243	13	81.2	173	18	US-10-425-115-91370	Sequence 91370, A	C 316	13	81.2	604	17	US-10-027-632-61763	Sequence 61763, A
C 244	13	81.2	193	17	US-10-424-599-12718	Sequence 12718, A	C 317	13	81.2	604	17	US-10-027-632-61764	Sequence 61764, A
C 245	13	81.2	201	19	US-10-741-600-56418	Sequence 56418, A	C 318	13	81.2	604	17	US-10-027-632-309949	Sequence 309949, A
C 246	13	81.2	207	9	US-09-738-626-2722	Sequence 2722, Ap	C 319	13	81.2	604	17	US-10-027-632-309950	Sequence 309950, A
C 247	13	81.2	223	17	US-10-424-599-53494	Sequence 53494, A	C 320	13	81.2	608	18	US-10-021-323-12795	Sequence 12795, A
C 248	13	81.2	228	16	US-10-029-386-27160	Sequence 27160, A	C 321	13	81.2	610	13	US-10-027-632-284833	Sequence 284833, A
C 249	13	81.2	231	18	US-10-723-860-4684	Sequence 4684, Ap	C 322	13	81.2	610	17	US-10-027-632-284833	Sequence 284833, A
C 250	13	81.2	240	9	US-09-864-761-21097	Sequence 21097, A	C 323	13	81.2	618	17	US-10-027-632-238664	Sequence 238664, A
C 251	13	81.2	286	18	US-10-425-115-5630	Sequence 5630, Ap	C 324	13	81.2	618	17	US-10-027-632-238664	Sequence 238664, A
C 252	13	81.2	289	17	US-10-702-075-261	Sequence 261, App	C 325	13	81.2	626	13	US-10-027-632-306191	Sequence 306191, A
C 253	13	81.2	291	17	US-10-424-599-95428	Sequence 95428, A	C 326	13	81.2	626	17	US-10-027-632-306191	Sequence 306191, A
C 254	13	81.2	308	17	US-10-424-599-107810	Sequence 107810, A	C 327	13	81.2	627	17	US-10-027-632-287327	Sequence 287327, A
C 255	13	81.2	339	18	US-10-723-860-884	Sequence 884, App	C 328	13	81.2	627	17	US-10-027-632-287327	Sequence 287327, A
C 256	13	81.2	343	9	US-09-960-352-7887	Sequence 7887, App	C 329	13	81.2	634	17	US-10-027-632-218555	Sequence 218555, A
C 257	13	81.2	365	17	US-10-113-664A-114	Sequence 114, App	C 330	13	81.2	634	17	US-10-027-632-218555	Sequence 218555, A
C 258	13	81.2	370	17	US-10-424-599-127598	Sequence 127598, A	C 331	13	81.2	640	13	US-10-027-632-125685	Sequence 125685, A
C 259	13	81.2	378	18	US-10-425-115-100567	Sequence 100567, A	C 332	13	81.2	640	13	US-10-027-632-125686	Sequence 125686, A
C 260	13	81.2	394	10	US-09-918-995-12878	Sequence 12878, A	C 333	13	81.2	640	13	US-10-027-632-125687	Sequence 125687, A
C 261	13	81.2	416	18	US-10-357-930-62003	Sequence 62003, A	C 334	13	81.2	640	17	US-10-027-632-125685	Sequence 125685, A
C 262	13	81.2	416	18	US-10-357-930-62038	Sequence 62038, A	C 335	13	81.2	640	17	US-10-027-632-125686	Sequence 125686, A
C 263	13	81.2	416	18	US-10-357-930-62136	Sequence 62136, A	C 336	13	81.2	640	17	US-10-027-632-125687	Sequence 125687, A
C 264	13	81.2	416	18	US-10-357-930-62195	Sequence 62195, A	C 337	13	81.2	642	17	US-10-282-122A-127561	Sequence 27561, A
C 265	13	81.2	420	9	US-09-933-797-450	Sequence 450, App	C 338	13	81.2	651	13	US-10-027-632-231754	Sequence 231754, A
C 266	13	81.2	423	17	US-10-027-632-88180	Sequence 88180, A	C 339	13	81.2	651	17	US-10-027-632-231754	Sequence 231754, A
C 267	13	81.2	423	17	US-10-027-632-88180	Sequence 88180, A	C 340	13	81.2	651	17	US-08-961-527-358	Sequence 358, App
C 268	13	81.2	427	9	US-09-867-701-5611	Sequence 5611, App	C 341	13	81.2	653	17	US-10-158-884-358	Sequence 358, App
C 269	13	81.2	446	18	US-10-425-115-51256	Sequence 51256, A	C 342	13	81.2	654	18	US-10-437-963-6623	Sequence 6623, App
C 270	13	81.2	446	18	US-10-767-701-16816	Sequence 16816, A	C 343	13	81.2	663	13	US-10-027-632-180652	Sequence 180652, A
C 271	13	81.2	449	9	US-09-864-761-4346	Sequence 4346, App	C 344	13	81.2	663	17	US-10-027-632-180652	Sequence 180652, A
C 272	13	81.2	453	18	US-10-373-963-8900	Sequence 8900, App	C 345	13	81.2	666	18	US-10-425-115-168808	Sequence 168808, A
C 273	13	81.2	454	10	US-09-918-995-22649	Sequence 22649, A	C 346	13	81.2	668	13	US-10-027-632-224984	Sequence 224984, A
C 274	13	81.2	464	9	US-09-864-761-1827	Sequence 1827, App	C 347	13	81.2	668	17	US-10-027-632-224984	Sequence 224984, A
C 275	13	81.2	465	13	US-10-027-632-268692	Sequence 268692, A	C 348	13	81.2	670	18	US-10-425-115-172633	Sequence 172633, A
C 276	13	81.2	465	17	US-10-027-632-268692	Sequence 268692, A	C 349	13	81.2	679	18	US-10-425-115-119888	Sequence 119888, A
C 277	13	81.2	469	18	US-10-425-115-109565	Sequence 109565, A	C 350	13	81.2	681	19	US-10-472-928-4127	Sequence 4127, App
C 278	13	81.2	469	18	US-10-357-930-58384	Sequence 58384, A	C 351	13	81.2	689	13	US-10-027-632-237921	Sequence 237921, A
C 279	13	81.2	474	10	US-09-918-995-28933	Sequence 28933, A	C 352	13	81.2	689	17	US-10-027-632-237921	Sequence 237921, A
C 280	13	81.2	478	10	US-09-918-995-1071	Sequence 1071, App	C 353	13	81.2	695	17	US-10-425-114-7387	Sequence 7387, App
C 281	13	81.2	487	18	US-10-021-323-6677	Sequence 6677, App	C 354	13	81.2	710	18	US-10-425-115-168803	Sequence 168803, A
C 282	13	81.2	488	17	US-10-424-599-76803	Sequence 76803, A	C 355	13	81.2	720	17	US-10-425-114-6357	Sequence 6357, App
C 283	13	81.2	489	18	US-10-437-963-56023	Sequence 56023, A	C 356	13	81.2	725	15	US-10-106-698-1657	Sequence 1657, App
C 284	13	81.2	490	17	US-10-424-599-55668	Sequence 55668, A	C 357	13	81.2	727	18	US-10-425-115-94463	Sequence 94463, A
C 285	13	81.2	498	10	US-09-918-995-11304	Sequence 11304, A	C 358	13	81.2	729	17	US-10-260-238-4417	Sequence 4417, App
C 286	13	81.2	503	10	US-09-918-995-28634	Sequence 28634, A	C 359	13	81.2	734	17	US-10-424-599-67163	Sequence 67163, A
C 287	13	81.2	516	19	US-10-696-639-2342	Sequence 2342, App	C 360	13	81.2	735	17	US-10-260-238-4418	Sequence 4418, App
C 288	13	81.2	519	13	US-10-027-632-275658	Sequence 275658, A	C 361	13	81.2	758	18	US-10-425-115-168805	Sequence 168805, A
C 289	13	81.2	519	18	US-10-027-632-275658	Sequence 275658, A	C 362	13	81.2	757	13	US-10-027-632-7332	Sequence 7332, App
C 290	13	81.2	519	18	US-10-021-323-12885	Sequence 12885, A	C 363	13	81.2	757	13	US-10-027-632-7332	Sequence 7332, App
C 291	13	81.2	526	18	US-10-021-323-12904	Sequence 12904, A	C 364	13	81.2	757	17	US-10-027-632-7332	Sequence 7332, App
C 292	13	81.2	530	18	US-10-425-115-109635	Sequence 109635, A	C 365	13	81.2	757	17	US-10-027-632-7332	Sequence 7332, App
C 293	13	81.2	530	18	US-10-425-115-151287	Sequence 151287, A	C 366	13	81.2	760	13	US-10-027-632-77187	Sequence 77187, A
C 294	13	81.2	533	13	US-10-027-632-193240	Sequence 193240, A	C 367	13	81.2	760	13	US-10-027-632-300355	Sequence 300355, A
C 295	13	81.2	533	17	US-10-027-632-193240	Sequence 193240, A	C 368	13	81.2	760	13	US-10-027-632-300356	Sequence 300356, A
C 296	13	81.2	537	16	US-10-029-386-13460	Sequence 13460, A	C 369	13	81.2	760	13	US-10-027-632-300357	Sequence 300357, A
C 297	13	81.2	539	18	US-10-653-047-2016	Sequence 2016, App	C 370	13	81.2	760	17	US-10-027-632-77187	Sequence 77187, A
C 298	13	81.2	555	13	US-10-027-632-43328	Sequence 43328, A	C 371	13	81.2	760	17	US-10-027-632-300355	Sequence 300355, A
C 299	13	81.2	555	13	US-10-027-632-43328	Sequence 43328, A	C 372	13	81.2	760	17	US-10-027-632-300356	Sequence 300356, A
C 300	13	81.2	555	17	US-10-027-632-43328	Sequence 43328, A	C 373	13	81.2	760	17	US-10-027-632-300357	Sequence 300357, A
C 301	13	81.2	555	17	US-10-027-632-43329	Sequence 43329, A	C 374	13	81.2	765	17	US-10-425-114-18617	Sequence 18617, A
C 302	13	81.2	565	18	US-10-021-323-3239	Sequence 3239, App	C 375	13	81.2	767	18	US-10-425-115-119920	Sequence 119920, A
C 303	13	81.2	567	18	US-10-021-323-13937	Sequence 13937, A	C 376	13	81.2	786	13	US-10-027-632-158263	Sequence 158263, A

377	13	81.2	786	17	US-10-027-632-158263	Sequence 158263,	450	13	81.2	1648	17	US-10-264-237-2844	Sequence 2844, Ap
378	13	81.2	810	13	US-10-027-632-131374	Sequence 131374,	451	13	81.2	1719	18	US-10-437-963-88744	Sequence 88744, Ap
379	13	81.2	810	13	US-10-027-632-131375	Sequence 131375,	452	13	81.2	1726	18	US-10-723-860-5470	Sequence 5470, Ap
380	13	81.2	810	17	US-10-027-632-131374	Sequence 131374,	453	13	81.2	1741	9	US-09-823-45A-350	Sequence 350, App
381	13	81.2	810	17	US-10-027-632-131375	Sequence 131375,	454	13	81.2	1759	13	US-10-027-632-97509	Sequence 97509, A
382	13	81.2	825	13	US-10-027-632-127197	Sequence 127197,	455	13	81.2	1769	17	US-09-814-335-21935	Sequence 21935, A
383	13	81.2	825	13	US-10-027-632-127198	Sequence 127198,	456	13	81.2	1781	13	US-10-027-632-97166	Sequence 97166, A
384	13	81.2	825	13	US-10-027-632-127198	Sequence 127198,	457	13	81.2	1781	13	US-10-027-632-100181	Sequence 100181, A
385	13	81.2	825	13	US-10-027-632-127198	Sequence 127198,	458	13	81.2	1781	13	US-10-027-632-100181	Sequence 100181, A
386	13	81.2	825	17	US-10-027-632-127197	Sequence 127197,	459	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
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388	13	81.2	825	17	US-10-027-632-173886	Sequence 173886,	461	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
389	13	81.2	827	13	US-10-027-632-174277	Sequence 174277,	462	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
390	13	81.2	827	13	US-10-027-632-174278	Sequence 174278,	463	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
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393	13	81.2	827	17	US-10-027-632-174279	Sequence 174279,	466	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
394	13	81.2	843	17	US-10-424-599-81460	Sequence 81460, A	467	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
395	13	81.2	870	17	US-10-424-599-67165	Sequence 67165, A	468	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
396	13	81.2	900	13	US-10-027-632-83045	Sequence 83045, A	469	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
397	13	81.2	900	13	US-10-027-632-83045	Sequence 83045, A	470	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
398	13	81.2	912	15	US-10-259-165-729	Sequence 729, App	471	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
399	13	81.2	912	15	US-10-326-185-98	Sequence 98, App1	472	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
400	13	81.2	912	17	US-10-260-238-5593	Sequence 5593, App	473	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
401	13	81.2	915	17	US-10-282-122A-38644	Sequence 38644, A	474	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
402	13	81.2	915	18	US-10-474-792-607	Sequence 607, App	475	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
403	13	81.2	931	17	US-10-374-780A-1380	Sequence 1380, App	476	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
404	13	81.2	933	17	US-10-425-114-6246	Sequence 6246, App	477	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
405	13	81.2	939	9	US-09-738-626-2678	Sequence 2678, App	478	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
406	13	81.2	939	13	US-10-027-632-381	Sequence 381, App	479	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
407	13	81.2	939	17	US-10-027-632-381	Sequence 381, App	480	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
408	13	81.2	960	13	US-10-027-632-255195	Sequence 255195,	481	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
409	13	81.2	960	17	US-10-027-632-255195	Sequence 255195,	482	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
410	13	81.2	978	17	US-10-116-275-287	Sequence 287, App	483	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
411	13	81.2	983	14	US-10-198-846-7285	Sequence 7285, App	484	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
412	13	81.2	991	17	US-10-424-599-74656	Sequence 74656, A	485	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
413	13	81.2	996	9	US-09-969-347-188	Sequence 188, App	486	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
414	13	81.2	996	19	US-10-843-641A-8317	Sequence 8317, App	487	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
415	13	81.2	1003	17	US-10-369-493-36884	Sequence 36884, A	488	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
416	13	81.2	1083	17	US-10-416-021-3	Sequence 3, App1	489	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
417	13	81.2	1095	9	US-09-925-298-183	Sequence 183, App	490	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
418	13	81.2	1095	14	US-10-102-806-183	Sequence 183, App	491	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
419	13	81.2	1110	17	US-10-369-493-26338	Sequence 26338, A	492	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
420	13	81.2	1137	17	US-10-425-114-29936	Sequence 29936, A	493	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
421	13	81.2	1150	18	US-10-767-701-11527	Sequence 11527, A	494	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
422	13	81.2	1170	17	US-10-282-122A-11956	Sequence 11956, A	495	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
423	13	81.2	1188	18	US-10-767-701-9171	Sequence 9171, App	496	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
424	13	81.2	1214	17	US-10-425-114-30965	Sequence 30965, A	497	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
425	13	81.2	1228	18	US-10-739-930-5138	Sequence 5138, App	498	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
426	13	81.2	1237	18	US-10-425-114-16955	Sequence 16955, A	499	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
427	13	81.2	1238	17	US-10-424-599-52932	Sequence 52932, A	500	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
428	13	81.2	1268	17	US-10-425-114-16955	Sequence 16955, A	501	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
429	13	81.2	1278	18	US-10-437-963-86593	Sequence 86593, A	502	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
430	13	81.2	1287	18	US-10-425-114-23328	Sequence 23328, A	503	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
431	13	81.2	1327	17	US-10-425-114-30528	Sequence 30528, A	504	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
432	13	81.2	1333	17	US-10-424-599-67166	Sequence 67166, A	505	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
433	13	81.2	1334	9	US-09-938-842A-5140	Sequence 5140, App	506	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
434	13	81.2	1344	11	US-09-938-842A-5140	Sequence 5140, App	507	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
435	13	81.2	1361	17	US-10-172-118-1124	Sequence 1124, App	508	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
436	13	81.2	1381	17	US-10-342-887-1124	Sequence 1124, App	509	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
437	13	81.2	1404	18	US-10-335-053-250	Sequence 250, App	510	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
438	13	81.2	1430	17	US-10-369-493-27052	Sequence 27052, A	511	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
439	13	81.2	1469	17	US-10-424-599-71810	Sequence 71810, A	512	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
440	13	81.2	1469	17	US-10-424-599-81461	Sequence 81461, A	513	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
441	13	81.2	1471	17	US-10-374-780A-480	Sequence 480, App	514	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
442	13	81.2	1471	17	US-10-412-699B-981	Sequence 981, App	515	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
443	13	81.2	1480	18	US-10-437-963-57554	Sequence 57554, App	516	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
444	13	81.2	1518	17	US-10-369-493-42629	Sequence 42629, A	517	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
445	13	81.2	1525	9	US-09-880-107-3816	Sequence 3816, App	518	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
446	13	81.2	1536	18	US-10-425-115-168810	Sequence 168810, A	519	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
447	13	81.2	1562	18	US-10-437-963-36491	Sequence 36491, A	520	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
448	13	81.2	1589	17	US-10-641-643-1405	Sequence 1405, App	521	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A
449	13	81.2	1629	17	US-10-641-643-528	Sequence 528, App	522	13	81.2	1781	17	US-10-027-632-97166	Sequence 97166, A

523	13	81.2	3872	18	US-10-437-963-57556	Sequence 57556, A	596	13	81.2	3309400	9	US-09-738-626-1	Sequence 1, Appl1
524	13	81.2	3984	18	US-10-437-963-14905	Sequence 14905, A	597	13	81.2	9025608	15	US-10-156-761-1	Sequence 1, Appl1
525	13	81.2	4027	16	US-10-252-157-464	Sequence 464, App	598	13	81.2	9025608	15	US-09-877-478-6174	Sequence 6174, App
526	13	81.2	4130	10	US-09-919-039-212	Sequence 212, App	599	13	81.2	9025608	15	US-10-342-902-6174	Sequence 6174, App
527	13	81.2	4181	17	US-10-149-736-43	Sequence 43, Appl1	600	13	81.2	9025608	15	US-10-669-841-2577	Sequence 2577, App
528	13	81.2	4181	19	US-10-964-536-43	Sequence 43, Appl1	601	13	81.2	9025608	15	US-09-940-244-179	Sequence 179, App
529	13	81.2	4361	16	US-10-240-965-13	Sequence 13, Appl1	602	13	81.2	9025608	15	US-09-940-244-184	Sequence 184, App
530	13	81.2	4403	9	US-09-880-107-2402	Sequence 2402, App	603	13	81.2	9025608	15	US-09-877-478-1149	Sequence 1149, App
531	13	81.2	4403	17	US-10-172-118-787	Sequence 787, App	604	13	81.2	9025608	15	US-09-864-638A-599	Sequence 599, App
532	13	81.2	4403	17	US-10-342-887-787	Sequence 787, App	605	13	81.2	9025608	15	US-09-864-638A-613	Sequence 613, App
533	13	81.2	4403	19	US-10-437-963-101126	Sequence 101126, App	606	13	81.2	9025608	15	US-09-864-638A-599	Sequence 599, App
534	13	81.2	5106	18	US-10-437-963-101126	Sequence 101126, App	607	13	81.2	9025608	15	US-09-864-426A-613	Sequence 613, App
535	13	81.2	5106	14	US-10-267-763-6	Sequence 6, Appl1	608	13	81.2	9025608	15	US-10-084-833-559	Sequence 559, App
536	13	81.2	5394	18	US-10-437-963-101130	Sequence 101130, App	609	13	81.2	9025608	15	US-10-084-833-613	Sequence 613, App
537	13	81.2	5608	9	US-09-962-436-259	Sequence 259, App	610	13	81.2	9025608	15	US-10-342-902-1149	Sequence 1149, App
538	13	81.2	5608	9	US-09-880-107-1760	Sequence 1760, App	611	13	81.2	9025608	15	US-10-356-861-179	Sequence 179, App
539	13	81.2	5608	19	US-10-843-641A-2718	Sequence 2718, App	612	13	81.2	9025608	15	US-10-356-861-184	Sequence 184, App
540	13	81.2	5676	18	US-10-437-963-101128	Sequence 101128, App	613	13	81.2	9025608	15	US-10-669-841-1149	Sequence 1149, App
541	13	81.2	5937	18	US-10-437-963-101135	Sequence 101135, App	614	13	81.2	9025608	15	US-10-309-584-184	Sequence 184, App
542	13	81.2	6006	18	US-10-437-963-101132	Sequence 101132, App	615	13	81.2	9025608	15	US-10-309-584-184	Sequence 184, App
543	13	81.2	6835	9	US-09-070-927A-204	Sequence 204, App	616	13	81.2	9025608	15	US-10-290-386-184	Sequence 184, App
544	13	81.2	7210	17	US-10-264-213-15	Sequence 15, Appl1	617	13	81.2	9025608	15	US-10-290-386-184	Sequence 184, App
545	13	81.2	8221	17	US-10-152-319A-2167	Sequence 2167, App	618	13	81.2	9025608	15	US-10-897-793-179	Sequence 179, App
546	13	81.2	9180	9	US-09-880-107-3461	Sequence 3461, App	619	13	81.2	9025608	15	US-10-897-793-184	Sequence 184, App
547	13	81.2	9180	18	US-10-723-860-4124	Sequence 4124, App	620	13	81.2	9025608	15	US-10-783-557-185	Sequence 185, App
548	13	81.2	10862	16	US-10-275-707-1	Sequence 1, Appl1	621	13	81.2	9025608	15	US-10-783-557-185	Sequence 185, App
549	13	81.2	10892	18	US-10-701-122-52	Sequence 52, App	622	13	81.2	9025608	15	US-09-940-244-180	Sequence 180, App
550	13	81.2	11839	10	US-09-764-891-7668	Sequence 7628, App	623	13	81.2	9025608	15	US-09-864-638A-614	Sequence 614, App
551	13	81.2	12566	8	US-08-961-527-149	Sequence 149, App	624	13	81.2	9025608	15	US-09-864-426A-614	Sequence 614, App
552	13	81.2	12566	17	US-10-158-844-149	Sequence 149, App	625	13	81.2	9025608	15	US-10-084-833-614	Sequence 614, App
553	13	81.2	15500	9	US-09-764-860-1091	Sequence 1091, App	626	13	81.2	9025608	15	US-10-244-647-56	Sequence 56, Appl1
554	13	81.2	15500	14	US-10-074-095-1091	Sequence 1091, App	627	13	81.2	9025608	15	US-10-244-647-702	Sequence 702, App
555	13	81.2	15500	17	US-10-212-872-1091	Sequence 1091, App	628	13	81.2	9025608	15	US-10-356-861-180	Sequence 180, App
556	13	81.2	15576	17	US-10-292-798-639	Sequence 639, App	629	13	81.2	9025608	15	US-10-309-584-180	Sequence 180, App
557	13	81.2	19994	15	US-10-017-161-728	Sequence 729, App	630	13	81.2	9025608	15	US-09-940-244-187	Sequence 187, App
558	13	81.2	27204	13	US-10-087-192-158	Sequence 1528, App	631	13	81.2	9025608	15	US-09-940-244-188	Sequence 188, App
559	13	81.2	28486	16	US-10-004-113-25	Sequence 25, Appl1	632	13	81.2	9025608	15	US-09-940-244-189	Sequence 189, App
560	13	81.2	28486	17	US-10-394-948-13	Sequence 13, Appl1	633	13	81.2	9025608	15	US-09-864-638A-607	Sequence 607, App
561	13	81.2	30781	14	US-10-092-908-37	Sequence 37, Appl1	634	13	81.2	9025608	15	US-09-864-638A-608	Sequence 608, App
562	13	81.2	34739	13	US-10-087-192-1846	Sequence 1846, App	635	13	81.2	9025608	15	US-09-864-638A-609	Sequence 609, App
563	13	81.2	37004	18	US-10-322-281-442	Sequence 442, App	636	13	81.2	9025608	15	US-09-864-426A-607	Sequence 607, App
564	13	81.2	37169	18	US-10-322-281-293	Sequence 293, App	637	13	81.2	9025608	15	US-09-864-426A-608	Sequence 608, App
565	13	81.2	42123	13	US-10-087-192-1588	Sequence 1588, App	638	13	81.2	9025608	15	US-09-864-426A-609	Sequence 609, App
566	13	81.2	44051	17	US-10-085-117-4	Sequence 4, Appl1	639	13	81.2	9025608	15	US-10-290-386-180	Sequence 180, App
567	13	81.2	50295	11	US-09-997-722-259	Sequence 259, App	640	13	81.2	9025608	15	US-10-032-589-5187	Sequence 5187, App
568	13	81.2	52211	13	US-10-087-192-1567	Sequence 1567, App	641	13	81.2	9025608	15	US-10-084-833-607	Sequence 607, App
569	13	81.2	53714	17	US-10-052-482-142	Sequence 142, App	642	13	81.2	9025608	15	US-10-084-833-608	Sequence 608, App
570	13	81.2	57347	18	US-10-322-281-317	Sequence 317, App	643	13	81.2	9025608	15	US-10-084-833-609	Sequence 609, App
571	13	81.2	71864	13	US-10-087-192-1927	Sequence 1927, App	644	13	81.2	9025608	15	US-10-356-861-187	Sequence 187, App
572	13	81.2	72069	19	US-10-741-600-17775	Sequence 17775, A	645	13	81.2	9025608	15	US-10-356-861-188	Sequence 188, App
573	13	81.2	73771	13	US-10-087-192-1636	Sequence 1636, App	646	13	81.2	9025608	15	US-10-356-861-189	Sequence 189, App
574	13	81.2	75252	13	US-10-087-192-904	Sequence 904, App	647	13	81.2	9025608	15	US-10-309-584-187	Sequence 187, App
575	13	81.2	80423	18	US-10-367-094-41	Sequence 41, Appl1	648	13	81.2	9025608	15	US-10-309-584-188	Sequence 188, App
576	13	81.2	87977	17	US-10-052-482-145	Sequence 145, Appl1	649	13	81.2	9025608	15	US-10-309-584-189	Sequence 189, App
577	13	81.2	92638	18	US-10-450-826-3	Sequence 3, Appl1	650	13	81.2	9025608	15	US-10-797-793-180	Sequence 180, App
578	13	81.2	97952	18	US-10-741-601-5646	Sequence 5646, App	651	13	81.2	9025608	15	US-10-893-557-181	Sequence 181, App
579	13	81.2	107036	18	US-10-322-281-756	Sequence 756, App	652	13	81.2	9025608	15	US-09-940-244-174	Sequence 174, App
580	13	81.2	147708	18	US-10-450-826-61	Sequence 61, Appl1	653	13	81.2	9025608	15	US-09-940-244-181	Sequence 181, App
581	13	81.2	177531	19	US-10-484-577-660	Sequence 660, App	654	13	81.2	9025608	15	US-09-940-244-186	Sequence 186, App
582	13	81.2	209484	13	US-10-087-192-418	Sequence 418, App	655	13	81.2	9025608	15	US-09-864-638A-600	Sequence 600, App
583	13	81.2	209484	18	US-10-331-053-4	Sequence 4, Appl1	656	13	81.2	9025608	15	US-09-864-638A-605	Sequence 605, App
584	13	81.2	233528	18	US-10-719-993-6856	Sequence 6856, App	657	13	81.2	9025608	15	US-09-864-638A-615	Sequence 615, App
585	13	81.2	269223	17	US-10-672-787-41	Sequence 41, Appl1	658	13	81.2	9025608	15	US-09-864-426A-605	Sequence 605, App
586	13	81.2	289190	18	US-10-322-281-115	Sequence 115, App	659	13	81.2	9025608	15	US-09-864-426A-605	Sequence 605, App
587	13	81.2	313287	18	US-10-322-281-48	Sequence 48, Appl1	660	13	81.2	9025608	15	US-09-864-426A-615	Sequence 615, App
588	13	81.2	313734	18	US-10-388-838-58	Sequence 58, Appl1	661	13	81.2	9025608	15	US-10-290-386-186	Sequence 186, App
589	13	81.2	392112	18	US-10-812-232-3	Sequence 3, Appl1	662	13	81.2	9025608	15	US-10-290-386-187	Sequence 187, App
590	13	81.2	430442	18	US-10-417-375-128	Sequence 128, App	663	13	81.2	9025608	15	US-10-290-386-188	Sequence 188, App
591	13	81.2	463122	13	US-10-087-192-226	Sequence 226, App	664	13	81.2	9025608	15	US-10-290-386-189	Sequence 189, App
592	13	81.2	717651	18	US-10-719-993-6817	Sequence 6817, App	665	13	81.2	9025608	15	US-10-084-833-600	Sequence 600, App
593	13	81.2	2162598	19	US-10-472-928-4879	Sequence 4879, App	666	13	81.2	9025608	15	US-10-084-833-605	Sequence 605, App
594	13	81.2	2840917	13	US-10-027-632-114763	Sequence 114763, App	667	13	81.2	9025608	15	US-10-084-833-615	Sequence 615, App
595	13	81.2	2940917	17	US-10-027-632-114763	Sequence 114763, App	668	13	81.2	9025608	15	US-10-084-833-615	Sequence 615, App

C 669	12	75.0	21	17	US-10-356-861-181	Sequence 181, App	742	12	75.0	41	16	US-10-084-833-597	Sequence 597, App
C 670	12	75.0	21	17	US-10-356-861-186	Sequence 186, App	743	12	75.0	41	17	US-10-356-861-183	Sequence 183, App
C 671	12	75.0	21	18	US-10-309-584-174	Sequence 174, App	744	12	75.0	41	18	US-10-309-584-183	Sequence 183, App
C 672	12	75.0	21	18	US-10-309-584-181	Sequence 181, App	745	12	75.0	42	16	US-10-290-386-183	Sequence 183, App
C 673	12	75.0	21	18	US-10-309-584-186	Sequence 186, App	746	12	75.0	43	18	US-10-897-793-183	Sequence 183, App
C 674	12	75.0	21	18	US-10-764-238-50	Sequence 50, App	747	12	75.0	43	19	US-10-783-557-184	Sequence 184, App
C 675	12	75.0	21	18	US-10-897-793-186	Sequence 186, App	748	12	75.0	53	19	US-10-677-9208-136	Sequence 136, App
C 676	12	75.0	21	18	US-10-897-793-187	Sequence 187, App	749	12	75.0	53	19	US-10-677-9208-136	Sequence 136, App
C 677	12	75.0	21	18	US-10-897-793-188	Sequence 188, App	750	12	75.0	65	19	US-10-677-9208-136	Sequence 136, App
C 678	12	75.0	21	18	US-10-897-793-189	Sequence 189, App	751	12	75.0	65	19	US-10-677-9208-136	Sequence 136, App
C 679	12	75.0	21	19	US-10-781-581-50	Sequence 50, App	752	12	75.0	119	17	US-10-424-599-14524	Sequence 4524, App
C 680	12	75.0	21	19	US-10-783-557-187	Sequence 187, App	753	12	75.0	150	18	US-10-767-701-15546	Sequence 15546, App
C 681	12	75.0	21	19	US-10-783-557-188	Sequence 188, App	754	12	75.0	160	17	US-10-242-538A-602	Sequence 602, App
C 682	12	75.0	21	19	US-10-783-557-189	Sequence 189, App	755	12	75.0	169	18	US-10-085-783A-602	Sequence 602, App
C 683	12	75.0	21	19	US-10-783-557-190	Sequence 190, App	756	12	75.0	169	18	US-10-437-963-32105	Sequence 32105, App
C 684	12	75.0	22	10	US-09-940-244-182	Sequence 182, App	757	12	75.0	183	18	US-10-425-115-164732	Sequence 164732, App
C 685	12	75.0	22	10	US-09-864-636A-616	Sequence 616, App	758	12	75.0	183	18	US-10-437-963-78559	Sequence 78559, App
C 686	12	75.0	22	11	US-09-864-636A-616	Sequence 616, App	759	12	75.0	183	18	US-10-437-963-78559	Sequence 78559, App
C 687	12	75.0	22	16	US-10-290-386-174	Sequence 174, App	760	12	75.0	186	18	US-10-425-115-79951	Sequence 79951, App
C 688	12	75.0	22	16	US-10-290-386-181	Sequence 181, App	761	12	75.0	188	18	US-10-425-115-79951	Sequence 79951, App
C 689	12	75.0	22	16	US-10-084-839-616	Sequence 616, App	762	12	75.0	188	18	US-10-425-115-77051	Sequence 77051, App
C 690	12	75.0	22	17	US-10-356-861-182	Sequence 182, App	763	12	75.0	189	9	US-09-923-876-4768	Sequence 4768, App
C 691	12	75.0	22	18	US-10-309-584-182	Sequence 182, App	764	12	75.0	190	18	US-10-425-115-28055	Sequence 28055, App
C 692	12	75.0	22	18	US-10-897-793-184	Sequence 184, App	765	12	75.0	190	18	US-10-425-115-28055	Sequence 28055, App
C 693	12	75.0	22	18	US-10-897-793-181	Sequence 181, App	766	12	75.0	201	18	US-10-741-601-14871	Sequence 14871, App
C 694	12	75.0	22	19	US-10-783-557-175	Sequence 175, App	767	12	75.0	201	18	US-10-741-601-14871	Sequence 14871, App
C 695	12	75.0	22	19	US-10-783-557-182	Sequence 182, App	768	12	75.0	201	18	US-10-741-601-14926	Sequence 14926, App
C 696	12	75.0	23	16	US-10-290-386-182	Sequence 182, App	769	12	75.0	201	18	US-10-741-601-14926	Sequence 14926, App
C 697	12	75.0	23	16	US-10-290-386-182	Sequence 182, App	770	12	75.0	201	18	US-10-741-601-14926	Sequence 14926, App
C 698	12	75.0	23	19	US-10-897-793-182	Sequence 183, App	771	12	75.0	201	19	US-10-719-993-37548	Sequence 37548, App
C 699	12	75.0	25	19	US-10-783-557-183	Sequence 183, App	772	12	75.0	201	19	US-10-719-993-37548	Sequence 37548, App
C 700	12	75.0	25	19	US-10-719-900-143951	Sequence 143951, App	773	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 701	12	75.0	25	19	US-10-719-900-810679	Sequence 810679, App	774	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 702	12	75.0	25	19	US-10-719-900-810679	Sequence 810679, App	775	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 703	12	75.0	25	19	US-10-809-189-49597	Sequence 49597, App	776	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 704	12	75.0	28	10	US-09-940-244-170	Sequence 170, App	777	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 705	12	75.0	28	10	US-09-940-244-175	Sequence 175, App	778	12	75.0	201	19	US-10-741-600-43528	Sequence 43528, App
C 706	12	75.0	28	10	US-09-940-244-185	Sequence 185, App	779	12	75.0	212	18	US-10-425-115-153228	Sequence 153228, App
C 707	12	75.0	28	10	US-09-864-636A-601	Sequence 601, App	780	12	75.0	212	18	US-10-674-124A-9948	Sequence 9948, App
C 708	12	75.0	28	10	US-09-864-636A-603	Sequence 603, App	781	12	75.0	219	9	US-10-027-632-270309	Sequence 270309, App
C 709	12	75.0	28	11	US-09-864-636A-611	Sequence 611, App	782	12	75.0	223	9	US-09-983-963-22298	Sequence 22298, App
C 710	12	75.0	28	11	US-09-864-426A-601	Sequence 601, App	783	12	75.0	223	18	US-10-437-963-79641	Sequence 79641, App
C 711	12	75.0	28	11	US-09-864-426A-603	Sequence 603, App	784	12	75.0	225	18	US-10-437-963-79641	Sequence 79641, App
C 712	12	75.0	28	11	US-09-864-426A-611	Sequence 611, App	785	12	75.0	235	18	US-10-425-115-16240	Sequence 16240, App
C 713	12	75.0	28	16	US-10-084-839-601	Sequence 601, App	786	12	75.0	240	9	US-10-437-963-30477	Sequence 30477, App
C 714	12	75.0	28	16	US-10-084-839-603	Sequence 603, App	787	12	75.0	241	17	US-09-867-701-6277	Sequence 6277, App
C 715	12	75.0	28	16	US-10-084-839-611	Sequence 611, App	788	12	75.0	253	9	US-10-424-599-135621	Sequence 135621, App
C 716	12	75.0	28	17	US-10-356-861-170	Sequence 170, App	789	12	75.0	253	18	US-10-425-115-177088	Sequence 177088, App
C 717	12	75.0	28	17	US-10-356-861-175	Sequence 175, App	790	12	75.0	257	9	US-09-867-701-7704	Sequence 7704, App
C 718	12	75.0	28	17	US-10-356-861-185	Sequence 185, App	791	12	75.0	257	9	US-09-867-701-10513	Sequence 10513, App
C 719	12	75.0	28	18	US-10-309-584-170	Sequence 170, App	792	12	75.0	258	16	US-10-125-159-86	Sequence 86, App
C 720	12	75.0	28	18	US-10-309-584-175	Sequence 175, App	793	12	75.0	258	16	US-10-437-963-71100	Sequence 71100, App
C 721	12	75.0	28	18	US-10-309-584-185	Sequence 185, App	794	12	75.0	261	18	US-10-437-963-16575	Sequence 60655, App
C 722	12	75.0	28	19	US-10-677-9208-137	Sequence 137, App	795	12	75.0	265	18	US-10-437-963-16575	Sequence 60655, App
C 723	12	75.0	28	19	US-10-677-9208-139	Sequence 139, App	796	12	75.0	266	9	US-10-425-115-157552	Sequence 157552, App
C 724	12	75.0	29	16	US-10-290-386-170	Sequence 299, App	797	12	75.0	266	18	US-09-783-550-81155	Sequence 4155, App
C 725	12	75.0	29	16	US-10-290-386-175	Sequence 170, App	798	12	75.0	266	18	US-10-674-124A-10968	Sequence 10968, App
C 726	12	75.0	29	16	US-10-290-386-185	Sequence 185, App	799	12	75.0	266	18	US-10-425-115-58800	Sequence 58800, App
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ALIGNMENTS

RESULT 1
US-09-888-164-29
Sequence 29, Application US/09888164
Publication No. US20030119724A1
GENERAL INFORMATION:
APPLICANT: Tsg'o, Paul O.P.
APPLICANT: Hangeland, Jon
APPLICANT: Deamond, Scott
APPLICANT: Roby, Clinton
TITLE OF INVENTION: LIGANDS TO ENHANCE CELLULAR UPTAKE OF BIOMOLECULES
FILE REFERENCE: 212241
CURRENT APPLICATION NUMBER: US/09/888, 164
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/282, 455
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 08/755, 062
PRIOR FILING DATE: 1996-11-22
PRIOR APPLICATION NUMBER: 60/007, 480
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Control oligomer
US-09-888-164-29

Query Match 100.0%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAAGCCACCCAGGCA 16
Db 1 AAAGCCACCCAGGCA 16

RESULT 2
US-10-453-792-41
Sequence 41, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453, 792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155, 885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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US-10-453-792-41
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RESULT 3
US-09-877-478-1755/c

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; Sequence 1755, Application US/09877478
; Publication No. US2003068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH80-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
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US-09-877-478-1755
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QY      1 AAAGCCACCCAGGCA 16
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Db       16 AAAGCCACCCAGGCA 1
```

```
RESULT 4
US-09-877-478-2378/c
; Sequence 2378, Application US/09877478
; Publication No. US2003068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH80-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
```

```
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2378
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-2378
```

```
Query Match          100.0%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAAGCCACCCAGGCA 16
        |||
Db       17 AAAGCCACCCAGGCA 2
```

```
RESULT 5
US-10-342-902-1755/c
; Sequence 1755, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH80-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-1755
```

```
Query Match          100.0%; Score 16; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAAGCCACCCAGGCA 16
        |||
Db       16 AAAGCCACCCAGGCA 1
```

```
RESULT 6
US-10-342-902-2378/c
; Sequence 2378, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
```

APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1993-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 2378
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-2378

Query Match 100.0%; Score 16; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 17 AAAGCCACCCAGGCA 2

RESULT 7
US-10-669-841-1755/c
Sequence 1755, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patricia, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 1755
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-669-841-1755

Query Match 100.0%; Score 16; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 16 AAAGCCACCCAGGCA 1

RESULT 8
US-10-669-841-2181/c
Sequence 2181, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patricia, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2181
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-669-841-2181

Query Match 100.0%; Score 16; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16

Db 17 AAAGCCACCCAGGCA 2

RESULT 9
US-10-453-792-49
; Sequence 49, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-453-792-49

Query Match 100.0%; Score 16; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
Db 1 AAAGCCACCCAGGCA 16

RESULT 10
US-10-244-647-54/C
; Sequence 54, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 54
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-244-647-54

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
Db 19 AAAGCCACCCAGGCA 4

RESULT 11
US-10-244-647-574/C
; Sequence 574, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-244-647-574

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
Db 17 AAAGCCACCCAGGCA 2

RESULT 12
US-10-244-647-576/c
; Sequence 576, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MEHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 576
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-576

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 16 AAAGCCACCCAGGCA 1

RESULT 13
US-10-244-647-577/c
; Sequence 577, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MEHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-577

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 18 AAAGCCACCCAGGCA 3

RESULT 14
US-10-244-647-700
; Sequence 700, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MEHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 700
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-700

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 1 AAAGCCACCCAGGCA 16

RESULT 15
US-10-244-647-1220
; Sequence 1220, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MEHB02-1000)
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1220
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1220

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 3 AAAGCCACCCAGGCA 18

RESULT 16
US-10-244-647-1222

Sequence 1222, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1222
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1222

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 4 AAAGCCACCCAGGCA 19

RESULT 17
US-10-244-647-1223

Sequence 1223, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647

CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1223
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1223

Query Match 100.0%; Score 16; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 2 AAAGCCACCCAGGCA 17

RESULT 18

US-10-244-647-1296/c
Sequence 1296, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US/10/244,647
PRIOR FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1296
LENGTH: 23
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-244-647-1296

Query Match 100.0%; Score 16; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
DB 23 AAAGCCACCCAGGCA 8

RESULT 19

US-09-756-500-4/c
Sequence 4, Application US/09756500
Patent No. US20010001098A1
GENERAL INFORMATION:
APPLICANT: Lu, Shan

APPLICANT: Huang, Zulu
APPLICANT: Herrmann, John E.
TITLE OF INVENTION: HEPATITIS B CORE ANTIGEN NUCLEIC ACID
FILE REFERENCE: 07917-077002
CURRENT APPLICATION NUMBER: US/09/756,500
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 09/400,497
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 60/101,311
PRIOR FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 54
TYPE: RNA
ORGANISM: Human Hepatitis B Virus
US-09-756-500-4

Query Match 100.0%; Score 16; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGCA 16
DB 43 AAAGCCACCCCAAGCA 28

RESULT 20
US-10-394-896-8/c
Sequence 8, Application US/10394896
Publication No. US20030235591A1
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
ADDRESSER: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/394,896
FILING DATE: MARCH 21, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8994
TELEFAX: (612) 334-8991
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 114 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-10-394-896-8

Query Match 100.0%; Score 16; DB 17; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGCA 16
DB 25 AAAGCCACCCCAAGCA 10

RESULT 21
US-10-394-896-11/c
Sequence 11, Application US/10394896
Publication No. US20030235591A1
GENERAL INFORMATION:
APPLICANT: Thoma, Hans
TITLE OF INVENTION: A Composition Used as a
TITLE OF INVENTION: Therapeutic Agent Against Chronic Viral Hepatic Diseases
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas Popovich
ADDRESSER: & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/394,896
FILING DATE: MARCH 21, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/075,520A
FILING DATE: January 31, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90124775
FILING DATE: December 19, 1990
APPLICATION NUMBER: PCT/EP91/02460
FILING DATE: December 19, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3757/MED1001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8994
TELEFAX: (612) 334-8991
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 bp
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-10-394-896-11

Query Match 100.0%; Score 16; DB 17; Length 291;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCCAAGCA 16
DB 25 AAAGCCACCCCAAGCA 10

RESULT 22

US-10-394-896-16/C

Sequence 16, Application US/10394896
Publication No. US20030235591A1

GENERAL INFORMATION:

APPLICANT: Thoma, Hans

TITLE OF INVENTION: A Composition Used as a

Therapeutic Agent Against Chronic Viral Hepatic Diseases

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thomas E. Popovich, Thomas Popovich

STREET: 80 South 8th Street

City: Minneapolis

STATE: Minnesota

COUNTRY: USA

ZIP: 55402-2111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible Compag Prolinea 4/66

OPERATING SYSTEM: MS-DOS Version 5

SOFTWARE: Microsoft Word for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/394,896

FILING DATE: MARCH 21, 2003

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/075,520A

FILING DATE: January 31, 1994

CLASSIFICATION:

APPLICATION NUMBER: EP 90124775

FILING DATE: December 19, 1990

APPLICATION NUMBER: PCT/EP91/02460

FILING DATE: December 19, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Thomas E. Popovich

REGISTRATION NUMBER: 30099

REFERENCE/DOCKET NUMBER: 3757/MED1001US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 334-8991

TELEFAX: (612) 334-8994

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 390 bp

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-10-394-896-16

Query Match

Best Local Similarity 100.0%; Score 16; DB 17; Length 390;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16

DB 25 AAAGCCACCCAGGCA 10

US-10-394-896-4/C

Sequence 4, Application US/10394896

Publication No. US20030235591A1

GENERAL INFORMATION:

APPLICANT: Thoma, Hans

TITLE OF INVENTION: A Composition Used as a

Therapeutic Agent Against Chronic Viral Hepatic Diseases

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thomas E. Popovich, Thomas Popovich

ADDRESSEE: & Associates

STREET: 80 South 8th Street

City: Minneapolis

STATE: Minnesota

COUNTRY: USA

ZIP: 55402-2111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible Compag Prolinea 4/66

OPERATING SYSTEM: MS-DOS Version 5

SOFTWARE: Microsoft Word for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/394,896

FILING DATE: MARCH 21, 2003

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/075,520A

FILING DATE: January 31, 1994

CLASSIFICATION:

APPLICATION NUMBER: EP 90124775

FILING DATE: December 19, 1990

APPLICATION NUMBER: PCT/EP91/02460

FILING DATE: December 19, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Thomas E. Popovich

REGISTRATION NUMBER: 30099

REFERENCE/DOCKET NUMBER: 3757/MED1001US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 334-8991

TELEFAX: (612) 334-8994

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 534 bp

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-10-394-896-4

Query Match

Best Local Similarity 100.0%; Score 16; DB 17; Length 534;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16

DB 25 AAAGCCACCCAGGCA 10

US-10-394-896-5/C

Sequence 5, Application US/10394896

Publication No. US20030235591A1

GENERAL INFORMATION:

APPLICANT: Thoma, Hans

TITLE OF INVENTION: A Composition Used as a

Therapeutic Agent Against Chronic Viral Hepatic Diseases

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thomas E. Popovich, Thomas Popovich

STREET: 80 South 8th Street

City: Minneapolis

STATE: Minnesota

COUNTRY: USA

ZIP: 55402-2111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible Compag Prolinea 4/66

OPERATING SYSTEM: MS-DOS Version 5

SOFTWARE: Microsoft Word for Windows

CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/10/394,896
; FILING DATE: MARCH 21, 2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,520A
; FILING DATE: January 31, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124775
; FILING DATE: December 19, 1990
; APPLICATION NUMBER: PCT/EP91/02460
; FILING DATE: December 19, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; REFERENCE/DOCKET NUMBER: 3757/MED1001US
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-10-394-896-5

```

```

Query Match      100.0%; Score 16; DB 17; Length 534;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AAAGCCACCCAGGCA 16
        |||||
Db      25 AAAGCCACCCAGGCA 10

```

```

RESULT 25
US-10-478-633A-69/C
; Sequence 69, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 69
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Hepatitis B virus
;
US-10-478-633A-69

```

```

Query Match      100.0%; Score 16; DB 19; Length 560;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AAAGCCACCCAGGCA 16
        |||||
Db      529 AAAGCCACCCAGGCA 514

```

```

RESULT 26
US-10-478-633A-70/C
; Sequence 70, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.

```

```

; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 70
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Hepatitis B virus
;
US-10-478-633A-70

```

```

Query Match      100.0%; Score 16; DB 19; Length 560;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AAAGCCACCCAGGCA 16
        |||||
Db      529 AAAGCCACCCAGGCA 514

```

```

RESULT 27
US-10-394-896-35/C
; Sequence 35, Application US/10394896
; Publication No. US2003023591A1
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans
; TITLE OF INVENTION: A Composition Used as a
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas Popovich
; ADDRESSEE: & Associates
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible Compaq Prolinea 4/66
; OPERATING SYSTEM: MS-DOS Version 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/394,896
; FILING DATE: MARCH 21, 2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,520A
; FILING DATE: January 31, 1994.
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124775
; FILING DATE: December 19, 1990
; APPLICATION NUMBER: PCT/EP91/02460
; FILING DATE: December 19, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; REFERENCE/DOCKET NUMBER: 3757/MED1001US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 588 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Single

```

TOPOLOGY: Linear
US-10-394-896-35

Query Match 100.0%; Score 16; DB 17; Length 588;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 25 AAAGCCACCCAGGCA 10

RESULT 28
US-10-312-045-1/c
Sequence 1, Application US/10312045
Publication No. US20040054139A1

GENERAL INFORMATION:
APPLICANT: Mark PAGE
APPLICANT: Jing-Li LI
APPLICANT: Paul PUMPHENS
APPLICANT: Galina BORISOVA
TITLE OF INVENTION: MODIFICATION OF HEPATITIS B CORE ANTIGEN
FILE REFERENCE: 117-432 / N78451B
CURRENT APPLICATION NUMBER: US/10/312,045
PCT/GB01/02817
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: PCT/GB01/02817
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: GB 0024544.9
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: GB 0015308.0
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 639
TYPE: DNA
ORGANISM: Hepatitis B virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(639)
US-10-312-045-1

Query Match 100.0%; Score 16; DB 17; Length 639;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 82 AAAGCCACCCAGGCA 67

RESULT 29
US-10-240-917-1/c
Sequence 1, Application US/10240917
Publication No. US2004023965A1
GENERAL INFORMATION:

APPLICANT: Annick GEHIN
APPLICANT: Robert GILBERT
APPLICANT: David STUART
APPLICANT: David ROWLANDS
TITLE OF INVENTION: HEPATITIS B CORE ANTIGEN FUSION PROTEINS
FILE REFERENCE: 117-419 / N79405B
CURRENT APPLICATION NUMBER: US/10/240,917
PCT/GB01/01607
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: PCT/GB01/01607
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: EP 00107118.2
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: MS Word
SEQ ID NO 1
LENGTH: 639
TYPE: DNA

ORGANISM: Hepatitis B virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(639)
US-10-240-917-1

Query Match 100.0%; Score 16; DB 18; Length 639;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 82 AAAGCCACCCAGGCA 67

RESULT 30
US-09-912-679-56/c
Sequence 56, Application US/09912679
Patent No. US20020141974A1

GENERAL INFORMATION:
APPLICANT: Jolly, Douglas J.
Lee, William T.L.
O'Dea, Joanne
Townsend, Kay
TITLE OF INVENTION: HEPATITIS THERAPEUTICS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/912,679
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.407C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-912-679-56

Query Match 100.0%; Score 16; DB 9; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||
DB 92 AAAGCCACCCAGGCA 77

RESULT 31
US-09-466-035-56/c
Sequence 56, Application US/09466035
Patent No. US20020165172A1

```

GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
MILICH, DAVID R.
LEE, WILLIAM T.I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INTRACELLULAR DISEASES
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Robins & Pasternak LLP
STREET: 545 Middlefield Road, Suite 180
CITY: Menlo Park
STATE: California
COUNTRY: U.S.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466,035
FILING DATE: 17-Dec-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pasternak, Danna S.
REGISTRATION NUMBER: 41,411
REFERENCE/DOCKET NUMBER: 2300-1231.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-325-7812
TELEFAX: 650-325-7823
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-466-035-56

Query Match      100.0%; Score 16; DB 9; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
DB      92 AAAGCCACCCCAAGCA 77

RESULT 32
US-09-821-662-23/C
; Sequence 23, Application US/09821662
; Publication No. US20040063652A1
; GENERAL INFORMATION:
; APPLICANT: JOLLY, Douglas J.
; Montisano, Dominic
; TITLE OF INVENTION: COMBINATION GENE DELIVERY VEHICLE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/821,662
; FILING DATE: 29-Mar-2001

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CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 930049.428
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-821-662-23

Query Match      100.0%; Score 16; DB 11; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
DB      92 AAAGCCACCCCAAGCA 77

RESULT 33
US-10-398-221-3305
; Sequence 3305, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3305
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Listeria monocytogenes 4b
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3305

Query Match      100.0%; Score 16; DB 17; Length 1841;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAAGCCACCCCAAGCA 16
DB      105 AAAGCCACCCCAAGCA 120

RESULT 34
US-10-461-790-97/C
; Sequence 97, Application US/10461790
; Publication No. US20040029111A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffery M.
; APPLICANT: Kolik, Daniel P.

```

APPLICANT: Dockter, Janel M.
APPLICANT: Getman, Damon K.
APPLICANT: Yoshimura, Tadashi
APPLICANT: Ho-Sing-Ioy, Marcy
APPLICANT: Stringfellow, Leslie A.
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GP134-02.UT
CURRENT APPLICATION NUMBER: US/10/461,790
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: 60/389,393
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 97
LENGTH: 1977
TYPE: DNA
ORGANISM: Hepatitis B virus
US-10-461-790-97

Query Match 100.0%; Score 16; DB 17; Length 1977;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 1883 AAAGCCACCCAGGCA 1868

RESULT 35
US-10-453-792-301/c
Sequence 301, Application US/10453792
Publication No. US20040029110A1

GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN

ROSSAU, RUDI

MAERTENS, GEBERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

NUMBER OF SEQUENCES: 313

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/453,792

FILING DATE: 04-Jun-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,885A

FILING DATE: 08-Oct-1998

APPLICATION NUMBER: PCT/EP97/02002

FILING DATE: 21-APR-1997

APPLICATION NUMBER: EP 96870053.4

FILING DATE: 19-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 2551-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 301:

SEQUENCE CHARACTERISTICS:

LENGTH: 3161 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 301:
US-10-453-792-301

Query Match 100.0%; Score 16; DB 17; Length 3161;
Best Local Similarity 100.0%; Pred. No. 5.3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 1876 AAAGCCACCCAGGCA 1861

RESULT 36
US-09-929-955-14/c
Sequence 14, Application US/09929955
Patent No. US20020136740A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg

APPLICANT: Catharina Hultgren

TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND

FILE REFERENCE: TRIPEP.23AUS2

CURRENT APPLICATION NUMBER: US/09/929,955

CURRENT FILING DATE: 2001-08-15

PRIOR APPLICATION NUMBER: 09/705,547

PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: 60/229,175

PRIOR FILING DATE: 2000-08-29

PRIOR APPLICATION NUMBER: 60/225,767

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 3182

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Hepatitis B virus sequence

US-09-929-955-14

Query Match 100.0%; Score 16; DB 9; Length 3182;

Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16

Db 1897 AAAGCCACCCAGGCA 1882

RESULT 37
US-10-104-966-14/c
Sequence 14, Application US/10104966
Publication No. US20020155124A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg

APPLICANT: Catharina Hultgren

TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND

FILE REFERENCE: TRIPEP.23AUS2

CURRENT APPLICATION NUMBER: US/10/104,966

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/705,547

PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: 60/229,175

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 3182
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hepatitis B virus sequence
US-10-104-966-14

Query Match 100.0%; Score 16; DB 13; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCACCAAGCA 16
DB 1897 AAAGCACCACCAAGCA 1882

RESULT 38
US-10-453-792-302/c
Sequence 302, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 302:
US-10-453-792-302

Query Match 100.0%; Score 16; DB 17; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCACCACCAAGCA 16

DB 1897 AAAGCACCACCAAGCA 1882

RESULT 39
US-10-453-792-303/c
Sequence 303, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 303:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 303:
US-10-453-792-303

Query Match 100.0%; Score 16; DB 17; Length 3182;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCACCAAGCA 16
DB 1897 AAAGCACCACCAAGCA 1882

RESULT 40
US-10-453-792-304/c
Sequence 304, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 304:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 304:
US-10-453-792-304
Query Match 100.0%; Score 16; DB 17; Length 3182;
Best Local Similarity 100.0%; Pred No. 5.2; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCCAAGCA 16
DB 1897 AAAGCCACCCCAAGCA 1882

Search completed: March 31, 2005, 14:14:42
Job time : 298 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:05:43 ; Search time 1558 Seconds
(without alignments)
390.904 Million cell updates/sec

Title: US-09-888-164-29

Perfect score: 16

Sequence: 1 aaagcaccacgaagca 16

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 66479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_mtc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g661.*
9: gb_g662.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	384	2	BF327943 QVQ-BN014
2	16	100.0	396	4	BI049449 CM2-GN022
3	16	100.0	441	9	CE327035 t1gr-g88-
4	16	100.0	464	1	AA103554 mo24h10.r1
5	16	100.0	496	2	BB144757 CM0-HT018
6	16	100.0	587	7	CF755881 DSAFL_2.1
7	16	100.0	623	5	BQ385327 NISC_mn11
8	16	100.0	646	6	CA192813 SCLSB104
9	16	100.0	659	2	BB545848 BB545848
10	16	100.0	666	6	CA083440 SCEPAM200
11	16	100.0	700	1	AV359761 AV359761
12	16	100.0	770	6	CD778583 EST64944
13	16	100.0	895	4	BI250824 G02993444
14	16	100.0	975	6	CA474404 AGENCOUR
15	16	100.0	987	7	W34362 ma99b12.r1
16	16	100.0	1684	9	CG754259 P049-3-E1
17	16	100.0	2005	3	AK009491 Mus musc
18	16	100.0	2368	3	AK078669 Mus musc
19	15	93.8	231	2	BB198017 BB198017
20	15	93.8	268	2	BF924007 CM2-NT01
21	15	93.8	285	2	BB090939 BB090939
22	15	93.8	287	2	BB309456 BB309456
23	15	93.8	294	7	W40391 zc80e10.r1
24	15	93.8	306	4	BI036238 CM3-NT024

25	15	93.8	310	2	BB251202
26	15	93.8	323	1	AI812549
27	15	93.8	328	1	AW921312
28	15	93.8	352	2	BP935524
29	15	93.8	365	7	CV001930
30	15	93.8	375	6	CB691996
31	15	93.8	394	6	CE698527 t1gr-g88-
32	15	93.8	401	9	CE047936 t1gr-g88-
33	15	93.8	408	4	BI536031 390188.MA
34	15	93.8	417	1	AA053186
35	15	93.8	419	5	BQ198462
36	15	93.8	423	1	AA147417
37	15	93.8	448	7	CN125873
38	15	93.8	455	6	CA902085
39	15	93.8	459	1	AA205003
40	15	93.8	465	8	BZ180217
41	15	93.8	499	7	CF477353
42	15	93.8	502	9	CE812092
43	15	93.8	509	6	CA902086
44	15	93.8	511	4	BG982671
45	15	93.8	513	9	CE514588
46	15	93.8	514	9	CE258762
47	15	93.8	514	9	CE603007
48	15	93.8	515	4	BG691107
49	15	93.8	525	6	CA394047
50	15	93.8	530	8	AZ835303
51	15	93.8	542	6	CA193115
52	15	93.8	543	4	BM669271
53	15	93.8	548	4	BM717229
54	15	93.8	549	9	CL184460
55	15	93.8	551	4	BM693039
56	15	93.8	553	4	Bj676120
57	15	93.8	556	1	AA131157
58	15	93.8	558	1	AA121607
59	15	93.8	558	9	CE357759
60	15	93.8	575	2	BB187673
61	15	93.8	587	6	CA902088
62	15	93.8	588	7	CF669528
63	15	93.8	594	5	B0198426
64	15	93.8	604	9	CE041883
65	15	93.8	606	2	BE566668
66	15	93.8	606	4	Bj258115
67	15	93.8	607	8	AZ438519
68	15	93.8	608	6	CD733924
69	15	93.8	619	7	CF512619
70	15	93.8	623	9	CE304273
71	15	93.8	627	7	CF476778
72	15	93.8	627	9	CL412826
73	15	93.8	628	4	BG436842
74	15	93.8	639	6	CA293504
75	15	93.8	640	6	CD718076
76	15	93.8	640	6	CD719040
77	15	93.8	641	5	BUT730169
78	15	93.8	655	6	CA145658
79	15	93.8	656	6	CA902087
80	15	93.8	662	9	CE333955
81	15	93.8	666	2	BB619841
82	15	93.8	666	4	Bj263735
83	15	93.8	666	9	AG134513
84	15	93.8	669	6	CA191351
85	15	93.8	673	6	CA131063
86	15	93.8	674	6	CA817866
87	15	93.8	676	6	CA132259
88	15	93.8	676	9	CL601784
89	15	93.8	677	6	CD718015
90	15	93.8	680	6	CA190702
91	15	93.8	682	6	CA815948
92	15	93.8	694	4	CE214848
93	15	93.8	707	9	CR046007
94	15	93.8	707	6	CB339361
95	15	93.8	719	2	BB191088
96	15	93.8	720	9	CL574012
97	15	93.8	733	7	CV036218

BB251202	BB251202
AI812549	I2G1_Pine
AW921312	ESW352616
BP935524	IL2-NT020
CV001930	G8A02-2MB
CB691996	AMGANNUC:S
CE698527	t1gr-g88-
CE047936	t1gr-g88-
BI536031	390188.MA
AA053186	2172404.r
BQ198462	NX1V131.E
AA147417	z039e07.r
CN125873	RHOH1_13
CA902085	PCS04356
AA205003	z072e12.r
BZ180217	CH230-485
CF477353	RTWV3_7_B
CE812092	t1gr-g88-
CA902086	PCS10343
BG982671	IL5-CN006
CE514588	t1gr-g88-
CE258762	t1gr-g88-
CE603007	t1gr-g88-
BG691107	340141.BA
CA394047	CS46e08.Y
AZ835303	2M0129P23
CA193115	SCLAD104
BM669271	UI-E-DM1-
BM717229	UI-E-DM1-
CL184460	104_397_1
BM693039	UI-E-CX1-
Bj676120	Bj676120
AA131157	z016e05.r
AA121607	z078c02.r
CE357759	t1gr-g88-
BB187673	BB187673
CA902088	PCS18183
CF669528	RTCNT1_44
B0198426	NX1V130.G
CE041883	t1gr-g88-
BE566668	B01339617
Bj258115	Bj258115
AZ438519	1M0228109
CD733924	4046868.1
CF512619	CApud0003
CE304273	t1gr-g88-
CF476778	RTWV3_3_A
CL412826	PIC14_43
BG436842	602488630
CA293504	SCSGLV100
CD718076	VVR146B09
CD719040	VVR156H05
BUT730169	UI-E-CX1-
CA145658	SCSGRT206
CA902087	PCS15106
CE333955	t1gr-g88-
BB619841	BB619841
Bj263735	Bj263735
AG134513	Pan_trog1
CA191351	SCCCT2C0
CA131063	SCBFR1106
CA817866	CA12E1301
CA132259	SCBGR105
CL601784	OB_Ba007
CD718015	VVR145E02
CA190702	SCCCT1C0
CA815948	CA12E1301
CE214848	t1gr-g88-
CR046007	Reverse_S
CB339361	CA23E1031
BB191088	BB191088
CL574012	OB_Ba002
CV036218	RTNACL1_5

98	15	93.8	739	6	CA155715	SCBPR2300	171	14	87.5	208	1	AA077832	AA077832	7H02F11.C
99	15	93.8	749	6	CB341563	CB341563	172	14	87.5	249	6	CA539386	CA539386	C0278D06-
100	15	93.8	749	6	CB982258	CB982258	172	14	87.5	253	9	CE010333	CE010333	tlgr-g8s-
101	15	93.8	752	4	BG386245	BG386245	173	14	87.5	256	9	CL525427	CL525427	A00692.SA
102	15	93.8	757	6	CD712674	CD712674	174	14	87.5	258	2	CE853225	CE853225	tlgr-g8s-
103	15	93.8	758	5	BX909708	BX909708	175	14	87.5	259	2	BR324970	BR324970	tlgr-g8s-
104	15	93.8	761	7	CF404762	CF404762	176	14	87.5	265	7	H34170	H34170	EST110813.R
105	15	93.8	769	9	CF664787	CF664787	177	14	87.5	266	1	BI064090	BI064090	tlgr-g8s-
106	15	93.8	762	9	CN60158U	CN60158U	178	14	87.5	275	4	BI006155	BI006155	tlgr-g8s-
107	15	93.8	768	9	BZ612822	BZ612822	179	14	87.5	280	1	AA778889	AA778889	AV085884
108	15	93.8	769	6	CB341495	CB341495	180	14	87.5	283	1	AA778889	AA778889	AV085884
109	15	93.8	771	6	CB342237	CB342237	181	14	87.5	285	7	CN310641	CN310641	746812.8
110	15	93.8	791	7	CF206302	CF206302	182	14	87.5	290	2	BF433605	BF433605	tlgr-g8s-
111	15	93.8	792	7	CF210957	CF210957	183	14	87.5	292	2	BF000628	BF000628	tlgr-g8s-
112	15	93.8	797	7	CF210957	CF210957	184	14	87.5	298	2	BF000628	BF000628	tlgr-g8s-
113	15	93.8	800	7	CO170582	CO170582	185	14	87.5	298	4	BF000628	BF000628	tlgr-g8s-
114	15	93.8	801	5	BU107434	BU107434	186	14	87.5	298	4	BF000628	BF000628	tlgr-g8s-
115	15	93.8	805	7	CO159063	CO159063	187	14	87.5	298	4	BF000628	BF000628	tlgr-g8s-
116	15	93.8	808	7	CO159063	CO159063	188	14	87.5	298	4	BF000628	BF000628	tlgr-g8s-
117	15	93.8	811	7	CO159063	CO159063	189	14	87.5	298	4	BF000628	BF000628	tlgr-g8s-
118	15	93.8	811	7	CO159063	CO159063	190	14	87.5	298	4	BF000628	BF000628	tlgr-g8s-
119	15	93.8	815	7	CO247269	CO247269	191	14	87.5	301	2	BE703009	BE703009	tlgr-g8s-
120	15	93.8	828	7	CK180837	CK180837	192	14	87.5	301	2	BE703009	BE703009	tlgr-g8s-
121	15	93.8	835	6	CL537542	CL537542	193	14	87.5	303	2	BF760650	BF760650	tlgr-g8s-
122	15	93.8	848	7	CO367613	CO367613	194	14	87.5	307	7	N24556	N24556	tlgr-g8s-
123	15	93.8	852	2	BF137430	BF137430	195	14	87.5	307	7	N24556	N24556	tlgr-g8s-
124	15	93.8	853	2	BE563709	BE563709	196	14	87.5	308	9	CG648100	CG648100	tlgr-g8s-
125	15	93.8	854	4	CF257869	CF257869	197	14	87.5	320	6	CD610797	CD610797	tlgr-g8s-
126	15	93.8	863	4	BG385624	BG385624	198	14	87.5	321	5	BO570588	BO570588	tlgr-g8s-
127	15	93.8	876	5	BU208515	BU208515	199	14	87.5	322	6	CD610798	CD610798	tlgr-g8s-
128	15	93.8	878	5	BU207838	BU207838	200	14	87.5	322	6	CD610798	CD610798	tlgr-g8s-
129	15	93.8	878	5	BO965349	BO965349	201	14	87.5	322	6	CD610798	CD610798	tlgr-g8s-
130	15	93.8	879	7	CO164380	CO164380	202	14	87.5	323	2	BE982287	BE982287	tlgr-g8s-
131	15	93.8	884	1	AU067735	AU067735	203	14	87.5	324	1	AA932175	AA932175	tlgr-g8s-
132	15	93.8	889	2	BE904092	BE904092	204	14	87.5	324	1	AA932175	AA932175	tlgr-g8s-
133	15	93.8	890	4	BG386850	BG386850	205	14	87.5	324	1	AA932175	AA932175	tlgr-g8s-
134	15	93.8	910	5	BO943147	BO943147	206	14	87.5	325	1	AA932175	AA932175	tlgr-g8s-
135	15	93.8	963	5	BO943147	BO943147	207	14	87.5	325	1	AA932175	AA932175	tlgr-g8s-
136	15	93.8	977	5	BO943147	BO943147	208	14	87.5	325	1	AA932175	AA932175	tlgr-g8s-
137	15	93.8	977	5	BO943147	BO943147	209	14	87.5	325	1	AA932175	AA932175	tlgr-g8s-
138	15	93.8	984	5	CL065453	CL065453	210	14	87.5	334	7	H29468	H29468	tlgr-g8s-
139	15	93.8	1031	9	CL083700	CL083700	211	14	87.5	335	1	AA169875	AA169875	tlgr-g8s-
140	15	93.8	1034	5	BQ054522	BQ054522	212	14	87.5	336	1	AA169875	AA169875	tlgr-g8s-
141	15	93.8	1091	8	CC212299	CC212299	213	14	87.5	338	1	AA437792	AA437792	tlgr-g8s-
142	15	93.8	1111	8	CC194571	CC194571	214	14	87.5	340	5	BY349097	BY349097	tlgr-g8s-
143	15	93.8	1164	6	CD507034	CD507034	215	14	87.5	341	1	AA628691	AA628691	tlgr-g8s-
144	15	93.8	1267	4	BF965185	BF965185	216	14	87.5	342	5	AA328838	AA328838	tlgr-g8s-
145	15	93.8	1267	4	BF965185	BF965185	217	14	87.5	342	5	AA328838	AA328838	tlgr-g8s-
146	15	93.8	1267	4	BF965185	BF965185	218	14	87.5	342	7	RI066872	RI066872	tlgr-g8s-
147	15	93.8	1270	3	AK039581	AK039581	219	14	87.5	344	1	AI648372	AI648372	tlgr-g8s-
148	15	93.8	1276	3	AK039581	AK039581	220	14	87.5	350	5	BY128036	BY128036	tlgr-g8s-
149	15	93.8	1276	3	AK039581	AK039581	221	14	87.5	350	9	CE669297	CE669297	tlgr-g8s-
150	15	93.8	1276	3	AK039581	AK039581	222	14	87.5	355	5	BY028627	BY028627	tlgr-g8s-
151	15	93.8	1276	3	AK039581	AK039581	223	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
152	15	93.8	1276	3	AK039581	AK039581	224	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
153	15	93.8	1276	3	AK039581	AK039581	225	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
154	15	93.8	1276	3	AK039581	AK039581	226	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
155	15	93.8	1276	3	AK039581	AK039581	227	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
156	15	93.8	1276	3	AK039581	AK039581	228	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
157	15	93.8	1276	3	AK039581	AK039581	229	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
158	15	93.8	1276	3	AK039581	AK039581	230	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
159	15	93.8	1276	3	AK039581	AK039581	231	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
160	15	93.8	1276	3	AK039581	AK039581	232	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
161	15	93.8	1276	3	AK039581	AK039581	233	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
162	15	93.8	1276	3	AK039581	AK039581	234	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
163	15	93.8	1276	3	AK039581	AK039581	235	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
164	15	93.8	1276	3	AK039581	AK039581	236	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
165	15	93.8	1276	3	AK039581	AK039581	237	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
166	15	93.8	1276	3	AK039581	AK039581	238	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
167	15	93.8	1276	3	AK039581	AK039581	239	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
168	15	93.8	1276	3	AK039581	AK039581	240	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
169	15	93.8	1276	3	AK039581	AK039581	241	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
170	15	93.8	1276	3	AK039581	AK039581	242	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-
171	15	93.8	1276	3	AK039581	AK039581	243	14	87.5	355	7	BY202241	BY202241	tlgr-g8s-

244	14	87.5	387	5	BY394941	BY394941	BY394941	317	14	87.5	458	5	BY263437	BY263437
245	14	87.5	387	7	UWC-pd3ov	CO991172	CO991172	318	14	87.5	459	1	AI086454	AI086454
246	14	87.5	388	1	AI892460	AI892460	mm10b10.y	319	14	87.5	459	1	AJ775688	AJ775688
247	14	87.5	388	4	BI257648	BI257648	602967570	320	14	87.5	459	9	CE657978	CE657978
248	14	87.5	392	1	AI358608	AI358608	6w40910.x	321	14	87.5	460	8	BH222284	1006106D0
249	14	87.5	392	2	BE702990	BE702990	RCS-NM108	322	14	87.5	462	5	BU972697	BH222284
250	14	87.5	392	5	BY308861	BY308861	BI308861	323	14	87.5	462	6	CF009087	CF009087
251	14	87.5	392	9	CE458523	CE458523	l1gr-g88-	324	14	87.5	462	6	BE671703	BE671703
252	14	87.5	393	6	BY578858	BY578858	LMAJFV1.1	325	14	87.5	464	1	AA014329	AA014329
253	14	87.5	396	6	BY578602	BY578602	BM746E02	326	14	87.5	464	1	AI858784	AI858784
254	14	87.5	397	2	AM150880	AM150880	xg41e03.x	327	14	87.5	464	7	W94439	W94439
255	14	87.5	398	9	CE510041	CE510041	l1gr-g88-	328	14	87.5	464	7	CE255220	CE255220
256	14	87.5	401	7	W88143	W88143	mf69c02.r1	329	14	87.5	465	7	W94254	W94254
257	14	87.5	404	2	AM168328	AM168328	x178c03.x	330	14	87.5	467	2	BE677543	BE677543
258	14	87.5	404	5	BY264309	BY264309	BY264309	331	14	87.5	467	6	CD874254	CD874254
259	14	87.5	405	6	CB811230	CB811230	AMGNNTC:S	332	14	87.5	468	2	BE049449	BE049449
260	14	87.5	406	6	CA004036	CA004036	H516F15r	333	14	87.5	469	1	AI923515	AI923515
261	14	87.5	407	8	BO3161	BO3161	CSRL-163H8-	334	14	87.5	469	9	CE096790	CE096790
262	14	87.5	409	9	CE448084	CE448084	l1gr-g88-	335	14	87.5	470	1	AI153827	AI153827
263	14	87.5	411	1	AI260456	AI260456	LP04328.3	336	14	87.5	470	2	AM182781	AM182781
264	14	87.5	411	1	AI590639	AI590639	tw24E01.x	337	14	87.5	471	7	R56230	R56230
265	14	87.5	412	5	BY056345	BY056345	BY056345	338	14	87.5	471	9	CE542973	CE542973
266	14	87.5	412	7	M68959	M68959	za70h09.r1	339	14	87.5	472	5	BO901314	BO901314
267	14	87.5	412	7	M62003	M62003	md83d03.r1	340	14	87.5	473	5	BO112058	BO112058
268	14	87.5	413	2	BF511227	BF511227	UI-H-B14-	341	14	87.5	474	2	BF063749	BF063749
269	14	87.5	414	1	AI087128	AI087128	oz75c01.x	342	14	87.5	475	1	AA259368	AA259368
270	14	87.5	414	2	BE326871	BE326871	hfe6908.x	343	14	87.5	475	7	R90558	R90558
271	14	87.5	416	1	AA644522	AA644522	af73d11.r	344	14	87.5	476	5	BY465943	BY465943
272	14	87.5	417	5	BY270421	BY270421	BY270421	345	14	87.5	477	1	AA495525	AA495525
273	14	87.5	417	9	CE306559	CE306559	l1gr-g88-	346	14	87.5	478	9	CE615388	CE615388
274	14	87.5	418	1	AA678335	AA678335	x116e01.8	347	14	87.5	481	1	AA106048	AA106048
275	14	87.5	418	1	AI871070	AI871070	w170c04.x	348	14	87.5	481	2	AM085524	AM085524
276	14	87.5	418	2	BE688256	BE688256	uw50f03.y	349	14	87.5	483	8	AZ877835	AZ877835
277	14	87.5	418	5	BY486629	BY486629	BY486629	350	14	87.5	483	9	CG671517	CG671517
278	14	87.5	419	7	W12858	W12858	mb16f12.r1	351	14	87.5	488	1	AA974025	AA974025
279	14	87.5	420	1	AA407226	AA407226	EST02221	352	14	87.5	488	1	AQ088025	AQ088025
280	14	87.5	422	1	AI325772	AI325772	mm10b10.y	353	14	87.5	491	1	AA927654	AA927654
281	14	87.5	422	1	AJ710865	AJ710865	AJ710865	354	14	87.5	491	1	AJ779076	AJ779076
282	14	87.5	423	5	BO599722	BO599722	MI-P-E6-a	355	14	87.5	491	5	BX645203	BX645203
283	14	87.5	423	6	CA809864	CA809864	CA221021	356	14	87.5	491	5	BY495357	BY495357
284	14	87.5	425	1	AA407137	AA407137	EST02121	357	14	87.5	491	9	CC830864	CC830864
285	14	87.5	426	8	BO2789	BO2789	CSRL-15g2-u	358	14	87.5	492	1	AA014622	AA014622
286	14	87.5	427	5	BY430071	BY430071	BY430071	359	14	87.5	492	7	CN310637	CN310637
287	14	87.5	429	2	BE500981	BE500981	7a33h09.x	360	14	87.5	492	8	BH269485	BH269485
288	14	87.5	430	6	CA568751	CA568751	K0432R03-	361	14	87.5	493	9	CE492773	CE492773
289	14	87.5	430	1	AA033054	AA033054	ml22a09.r	362	14	87.5	496	7	CF907776	CF907776
290	14	87.5	430	7	W64958	W64958	me04f12.r1	363	14	87.5	497	6	CD923425	CD923425
291	14	87.5	433	5	BY505197	BY505197	BY505197	364	14	87.5	498	1	AA466023	AA466023
292	14	87.5	433	8	AZ586226	AZ586226	IM0392B02	365	14	87.5	498	2	BE234847	BE234847
293	14	87.5	435	2	AQ813525	AQ813525	HS_5314.A	366	14	87.5	498	6	CA561977	CA561977
294	14	87.5	436	1	AI817667	AI817667	tdf5c06.x	367	14	87.5	498	6	CA656757	CA656757
295	14	87.5	436	2	AM468996	AM468996	hc74d11.x	368	14	87.5	499	2	BE851236	BE851236
296	14	87.5	437	7	W89731	W89731	mf66g06.r1	369	14	87.5	499	9	CE551084	CE551084
297	14	87.5	437	9	CR303758	CR303758	Medicago	370	14	87.5	500	2	BE195700	BE195700
298	14	87.5	440	2	AM136487	AM136487	UI-H-B11-	371	14	87.5	504	8	AQ303160	AQ303160
299	14	87.5	440	2	BB859094	BB859094	BB859094	372	14	87.5	505	8	AQ455482	AQ455482
300	14	87.5	441	1	AI859818	AI859818	mm20h02.x	373	14	87.5	508	4	BG144799	BG144799
301	14	87.5	442	8	AO353984	AO353984	RPCI-11-3	374	14	87.5	508	5	BY158097	BY158097
302	14	87.5	445	2	AM139790	AM139790	UI-H-B11-	375	14	87.5	510	1	AI994130	AI994130
303	14	87.5	445	8	BH858855	BH858855	S3_x022a2	376	14	87.5	512	8	BZ933197	BZ933197
304	14	87.5	447	2	AM206554	AM206554	UI-H-B11-	377	14	87.5	513	5	BX952471	BX952471
305	14	87.5	447	9	CE185885	CE185885	l1gr-g88-	378	14	87.5	514	5	BM573423	BM573423
306	14	87.5	450	1	AA638297	AA638297	v397d12.r	379	14	87.5	514	8	AZ639234	AZ639234
307	14	87.5	450	2	AM294117	AM294117	UI-H-B12-	380	14	87.5	514	8	BZ421173	BZ421173
308	14	87.5	450	2	BE109612	BE109612	UI-R-BJ1-	381	14	87.5	515	6	CD843769	CD843769
309	14	87.5	452	1	AI655930	AI655930	lt41f01.x	382	14	87.5	516	7	CF842185	CF842185
310	14	87.5	454	2	AM206668	AM206668	UI-H-B11-	383	14	87.5	520	1	BF001816	BF001816
311	14	87.5	454	5	BY277268	BY277268	BY277268	384	14	87.5	520	1	AI564801	AI564801
312	14	87.5	455	7	CF294659	CF294659	30DG5--04	385	14	87.5	520	1	AI885151	AI885151
313	14	87.5	456	7	R85051	R85051	yo40f09.r1	386	14	87.5	520	2	BF055065	BF055065
314	14	87.5	456	7	AA050812	AA050812	m722a06.r	387	14	87.5	520	2	CE617994	CE617994
315	14	87.5	456	6	CA559676	CA559676	K0261R07-	388	14	87.5	521	1	AA261718	AA261718
316	14	87.5	457	1	AI225804	AI225804	ut21c08.y	389	14	87.5	521	5	BQ832749	BQ832749

390	14	87.5	521	5	BU734867	UI-E-DW0-	463	14	87.5	580	5	BQ091430	TA02.19f0
391	14	87.5	523	2	BF433551	BF433551.7055a05.x	464	14	87.5	580	5	BQ092421	TA02.02a0
392	14	87.5	524	9	CE189596	t1gr-g8s-	465	14	87.5	581	5	BP252648	BP252648
393	14	87.5	526	1	AI527345	AI527345.UJ51a12.x	466	14	87.5	581	5	BQ092063	T302.07h0
394	14	87.5	527	2	BF594824	BF594824.7055h05.x	467	14	87.5	582	2	AM101904	BD72C05.Y
395	14	87.5	527	2	AM190802	AM190802.X165g12.x	468	14	87.5	582	5	BP271039	BP271039
396	14	87.5	529	7	CE674419	CE674419.t1gr-g8s-	469	14	87.5	582	5	BP288264	BP288264
397	14	87.5	529	7	CO595580	CO595580.D08-11k2	470	14	87.5	582	5	BP361364	BP361364
398	14	87.5	529	7	CR175354	CR175354.Forward.8	471	14	87.5	583	2	AM964954	AM964954.E8T736922
399	14	87.5	530	1	AL629513	AL629513	472	14	87.5	584	6	CD293216	SRTPU536.
400	14	87.5	531	6	CA603741	CA603741.wt1.pk003	473	14	87.5	586	1	AI145824	ME08c11.r
401	14	87.5	532	2	AV548987	AV548987	474	14	87.5	586	8	BH067631	RPTC1-24-2
402	14	87.5	532	2	BE591432	BE591432.WHE1659-1	475	14	87.5	587	1	AA141444	AA141444
403	14	87.5	532	7	HI7628	HI7628.YM40C06.81	476	14	87.5	587	1	AA141444	AA141444
404	14	87.5	534	7	CV355785	CV355785.MR4-KT004	477	14	87.5	587	1	AU056398	AU056398
405	14	87.5	535	6	CB718072	CB718072.AMGNTC:N	478	14	87.5	587	4	BM250087	K084AB06-
406	14	87.5	535	8	AQ058246	AQ058246.HS-2086_B	479	14	87.5	587	4	BM250087	K084AB06-
407	14	87.5	536	8	CE590031	CE590031.t1gr-g8s-	480	14	87.5	588	9	BQ295332	CE285790
408	14	87.5	537	1	AI603779	AI603779.486096G06	481	14	87.5	589	6	CD615344	CD615344
409	14	87.5	538	2	BF057394	BF057394.7K43C08.x	482	14	87.5	589	6	CD615344	CD615344
410	14	87.5	538	6	CB717477	CB717477.AMGNTC:N	483	14	87.5	589	7	M31110	M31110
411	14	87.5	539	9	CE850654	CE850654.t1gr-g8s-	484	14	87.5	591	1	AI464863	ME92d01.Y
412	14	87.5	541	5	BQ901739	BQ901739.Ta02_11b0	485	14	87.5	591	6	CAS60747	K0276G05-
413	14	87.5	541	7	CO684801	CO684801.DG11-190b	486	14	87.5	591	9	CE379196	t1gr-g8s-
414	14	87.5	541	9	CE678435	CE678435.t1gr-g8s-	487	14	87.5	595	2	BF494674	BF494674
415	14	87.5	542	2	BE244521	BE244521.TCBA2PD14	488	14	87.5	596	6	CA019764	HV13A18r
416	14	87.5	542	5	BO620649	BO620649.TaTr1136F	489	14	87.5	596	6	CD997943	CD997943
417	14	87.5	542	7	CF857710	CF857710.PEMY003id	490	14	87.5	597	9	CE199460	CE199460
418	14	87.5	543	1	AI111725	AI111725.mP54b09.r	491	14	87.5	598	2	BE982217	WHE1798_B
419	14	87.5	543	1	AI571347	AI571347.LH5a12.x	492	14	87.5	598	2	BE978594	BE978594
420	14	87.5	547	1	AI563989	AI563989.LM33C07.x	493	14	87.5	598	6	CA696693	CA696693
421	14	87.5	547	2	BF722838	BF722838.mB24d01.	494	14	87.5	600	4	BI987687	BI987687
422	14	87.5	548	1	AI610642	AI610642	495	14	87.5	600	9	CE137159	CE137159
423	14	87.5	549	5	BQ901379	BQ901379.Ta02_1891	496	14	87.5	600	9	CE233377	CE233377
424	14	87.5	550	5	BQ017394	BQ017394.UI-H-DT1.	497	14	87.5	601	9	CE388330	CE388330
425	14	87.5	551	8	AZ440782	AZ440782.1M023G01	498	14	87.5	601	9	CE575207	CE575207
426	14	87.5	552	1	AU143957	AU143957	499	14	87.5	603	9	CE243209	CE243209
427	14	87.5	552	7	CF906006	CF906006.A0441P02-	500	14	87.5	603	9	CE650456	CE650456
428	14	87.5	553	1	AV406141	AV406141	501	14	87.5	604	9	CE723170	CE723170
429	14	87.5	554	6	CA701608	CA701608.WKM2C.PK0	502	14	87.5	604	9	CE793923	CE793923
430	14	87.5	555	4	BG057682	BG057682.na111908.	503	14	87.5	605	2	BE310003	BE310003
431	14	87.5	556	9	CE105609	CE105609.t1gr-g8s-	504	14	87.5	606	9	CE351120	CE351120
432	14	87.5	557	7	CF982293	CF982293.ma3180c07.	505	14	87.5	607	2	BE583348	BE583348
433	14	87.5	558	7	CN008833	CN008833.WHE2645_F	506	14	87.5	607	4	BG087199	BG087199
434	14	87.5	559	9	CE804967	CE804967.t1gr-g8s-	507	14	87.5	608	4	AC306456	AC306456
435	14	87.5	560	6	CD635565	CD635565.56075940H	508	14	87.5	609	8	BC319748	BC319748
436	14	87.5	560	7	CF725721	CF725721.UI-M-GZ0-	509	14	87.5	609	7	CF904382	CF904382
437	14	87.5	565	9	CE804967	CE804967.t1gr-g8s-	510	14	87.5	609	7	CF904382	CF904382
438	14	87.5	566	2	BF026819	BF026819.UI-E-C10-	511	14	87.5	611	1	AI625072	AI625072
439	14	87.5	566	6	CD635565	CD635565.56075940H	512	14	87.5	611	9	CE193885	CE193885
440	14	87.5	567	2	CF725721	CF725721.UI-M-GZ0-	513	14	87.5	612	1	AA877325	AA877325
441	14	87.5	567	7	CF725721	CF725721.UI-M-GZ0-	514	14	87.5	613	7	CK347000	CK347000
442	14	87.5	568	4	BM255235	BM255235.516915_MA	515	14	87.5	615	6	CE272602	CE272602
443	14	87.5	568	4	BM255235	BM255235.516915_MA	516	14	87.5	616	6	BM590753	BM590753
444	14	87.5	568	4	BM255235	BM255235.516915_MA	517	14	87.5	616	6	BM590753	BM590753
445	14	87.5	568	4	BM255235	BM255235.516915_MA	518	14	87.5	616	6	BM590753	BM590753
446	14	87.5	568	4	BM255235	BM255235.516915_MA	519	14	87.5	616	6	BM590753	BM590753
447	14	87.5	568	4	BM255235	BM255235.516915_MA	520	14	87.5	616	6	BM590753	BM590753
448	14	87.5	568	4	BM255235	BM255235.516915_MA	521	14	87.5	616	6	BM590753	BM590753
449	14	87.5	568	4	BM255235	BM255235.516915_MA	522	14	87.5	616	6	BM590753	BM590753
450	14	87.5	568	4	BM255235	BM255235.516915_MA	523	14	87.5	616	6	BM590753	BM590753
451	14	87.5	568	4	BM255235	BM255235.516915_MA	524	14	87.5	616	6	BM590753	BM590753
452	14	87.5	568	4	BM255235	BM255235.516915_MA	525	14	87.5	616	6	BM590753	BM590753
453	14	87.5	568	4	BM255235	BM255235.516915_MA	526	14	87.5	616	6	BM590753	BM590753
454	14	87.5	568	4	BM255235	BM255235.516915_MA	527	14	87.5	616	6	BM590753	BM590753
455	14	87.5	568	4	BM255235	BM255235.516915_MA	528	14	87.5	616	6	BM590753	BM590753
456	14	87.5	568	4	BM255235	BM255235.516915_MA	529	14	87.5	616	6	BM590753	BM590753
457	14	87.5	568	4	BM255235	BM255235.516915_MA	530	14	87.5	616	6	BM590753	BM590753
458	14	87.5	568	4	BM255235	BM255235.516915_MA	531	14	87.5	616	6	BM590753	BM590753
459	14	87.5	568	4	BM255235	BM255235.516915_MA	532	14	87.5	616	6	BM590753	BM590753
460	14	87.5	568	4	BM255235	BM255235.516915_MA	533	14	87.5	616	6	BM590753	BM590753
461	14	87.5	568	4	BM255235	BM255235.516915_MA	534	14	87.5	616	6	BM590753	BM590753
462	14	87.5	568	4	BM255235	BM255235.516915_MA	535	14	87.5	616	6	BM590753	BM590753

536	14	87.5	630	6	CD931767	GR45.1151	609	14	87.5	698	9	CE622321	CE622321	l1gr-g88-
537	14	87.5	632	8	B2138683	CH230-387	610	14	87.5	699	2	BF497217	BF497217	AT11342.5
538	14	87.5	632	8	B2642803	OGMO69TC	611	14	87.5	699	2	BF984241	BF984241	UI-CF-ECL
539	14	87.5	633	1	AV826345	AV826345	612	14	87.5	700	7	CK567115	CK567115	HO05122W
540	14	87.5	634	5	BM971609	UI-CF-ECL	613	14	87.5	702	5	B0633147	B0633147	UI-H-FL1-
541	14	87.5	634	6	CA029583	H265K03r	614	14	87.5	703	5	BQ008775	BQ008775	UI-H-E10-
542	14	87.5	637	8	A2269017	RPCI-23-1	615	14	87.5	703	7	CF634435	CF634435	zmrw00_0
543	14	87.5	638	8	CE415077	l1gr-g88-	616	14	87.5	704	7	CO247483	CO247483	AGENCOURT
544	14	87.5	639	2	BB204409	BB204409	617	14	87.5	706	5	BQ000856	BQ000856	UI-H-DH1-
545	14	87.5	640	9	CR254497	Reverse	618	14	87.5	706	5	BX504413	BX504413	UI-H-DH1-
546	14	87.5	641	7	CF905263	A0432D08-	619	14	87.5	706	8	B2546589	B2546589	OGAKD05TM
547	14	87.5	644	5	BQ747303	UI-M-PA0-	620	14	87.5	707	9	CE728433	CE728433	l1gr-g88-
548	14	87.5	645	6	CA196182	SCSBAD108	621	14	87.5	710	5	BM980924	BM980924	UI-CF-ECL
549	14	87.5	645	9	CE767705	CH240_66D	622	14	87.5	710	6	CA423554	CA423554	UI-H-PE1-
550	14	87.5	645	9	CE573905	l1gr-g88-	623	14	87.5	710	6	CA427124	CA427124	UI-H-PE1-
551	14	87.5	646	2	BS598293	BS598293	624	14	87.5	712	9	CNS05P29	CNS05P29	AL348606
552	14	87.5	646	5	BQ46812	UI-H-EU1-	625	14	87.5	713	6	BY753072	BY753072	TEtraodon
553	14	87.5	646	5	B0732265	UI-E-CQ1-	626	14	87.5	714	9	CR143208	CR143208	Forward
554	14	87.5	646	6	CA311297	UI-CF-FNO	627	14	87.5	715	9	CNS03SVQ	AL259055	TEtraodon
555	14	87.5	646	6	CA436361	CA436361	628	14	87.5	715	9	CE213328	CE213328	l1gr-g88-
556	14	87.5	649	5	BU631088	BU631088	629	14	87.5	716	2	BF608303	BF608303	MY1_00124
557	14	87.5	649	6	CD927206	GR45_101E	630	14	87.5	716	5	BM981155	BM981155	UI-CF-ECL
558	14	87.5	650	7	CP294881	30DG5--04	631	14	87.5	716	5	BQ194023	BQ194023	UI-R-CN1-
559	14	87.5	650	7	CV006340	CS_g11_14	632	14	87.5	721	6	BF346081	BF346081	AGENCOURT
560	14	87.5	651	4	AA876227	AA876227	633	14	87.5	721	2	CNS05PXC	AL250654	TEtraodon
561	14	87.5	653	1	AA876227	AA876227	634	14	87.5	721	8	AZ250654	RPCI-23-9	AGENCOURT
562	14	87.5	653	6	CD931180	GR45_113L	635	14	87.5	722	8	AG485283	AG485283	602504336
563	14	87.5	654	6	CD931181	GR45_113L	636	14	87.5	723	4	BM971334	BM971334	UI-CF-ECL
564	14	87.5	657	2	BF631327	zmrw648_0	637	14	87.5	725	1	AL110416	AL110416	DKFZP434K
565	14	87.5	657	2	BF488258	AT23485_5	638	14	87.5	727	5	BM971334	BM971334	UI-CF-ECL
566	14	87.5	657	7	CF902322	CF902322	639	14	87.5	727	9	CE409035	CE409035	l1gr-g88-
567	14	87.5	658	5	B0004401	UI-H-E10-	640	14	87.5	727	7	CE409035	CE409035	l1gr-g88-
568	14	87.5	658	6	CB600291	CB600291	641	14	87.5	728	6	BI598138	BI598138	603253384
569	14	87.5	660	6	BY753686	BY753686	642	14	87.5	728	6	CD240976	CD240976	AGENCOURT
570	14	87.5	660	6	CA216538	SCCRL500	643	14	87.5	730	9	CC512431	CC512431	CH240_356
571	14	87.5	661	6	BY753669	BY753669	644	14	87.5	731	2	BF488931	BF488931	AT24603.5
572	14	87.5	662	2	BB624945	BB624945	645	14	87.5	731	7	CK474134	CK474134	AGENCOURT
573	14	87.5	663	6	BY753487	BY753487	646	14	87.5	733	7	CK476841	CK476841	AGENCOURT
574	14	87.5	663	6	CA135166	CA135166	647	14	87.5	734	7	CO430874	CO430874	UI-M-HX0-
575	14	87.5	663	7	CR413421	CR413421	648	14	87.5	734	9	CNS05NZ8	AL346013	TEtraodon
576	14	87.5	668	1	AL042531	AL042531	649	14	87.5	736	9	CC493248	CC493248	CH240_327
577	14	87.5	670	7	CN280352	CN280352	650	14	87.5	738	5	BQ207080	BQ207080	UI-R-D21-
578	14	87.5	671	1	AI048249	AI048249	651	14	87.5	739	9	CE817615	CE817615	l1gr-g88-
579	14	87.5	671	2	BE975003	BE975003	652	14	87.5	739	4	BG064967	BG064967	H3025H05-
580	14	87.5	671	6	BY753431	BY753431	653	14	87.5	740	7	CN211047	CN211047	RJA071A04
581	14	87.5	671	7	CN280354	CN280354	654	14	87.5	740	2	BF791564	BF791564	602251662
582	14	87.5	671	7	CN295840	CN295840	655	14	87.5	744	2	BF494210	BF494210	AT02648.5
583	14	87.5	676	2	BF620764	BF620764	656	14	87.5	744	6	CB601577	CB601577	AGENCOURT
584	14	87.5	676	5	BU609825	BU609825	657	14	87.5	744	9	AG372210	AG372210	M88_rubcu
585	14	87.5	677	1	AI405290	AI405290	658	14	87.5	745	4	BI751593	BI751593	Ta01_12h0
586	14	87.5	677	9	CE451616	CE451616	659	14	87.5	746	1	AA986905	AA986905	ue16d1.2.x
587	14	87.5	677	9	CE575299	CE575299	660	14	87.5	746	9	CNS056MT	CNS056MT	TEtraodon
588	14	87.5	677	9	CE630847	CE630847	661	14	87.5	747	7	CV077997	CV077997	AGENCOURT
589	14	87.5	677	9	BU615358	BU615358	662	14	87.5	749	4	BG416135	BG416135	HVSMEX000
590	14	87.5	680	7	CO043288	CO043288	663	14	87.5	749	5	BM945422	BM945422	UI-M-EMO-
591	14	87.5	681	9	CE218664	CE218664	664	14	87.5	749	7	CO403404	CO403404	AGENCOURT
592	14	87.5	682	8	BS503046	BS503046	665	14	87.5	750	5	BU239867	BU239867	603322274
593	14	87.5	682	8	AO415326	AO415326	666	14	87.5	750	5	BU633698	BU633698	UI-H-FL1-
594	14	87.5	684	6	BY754188	BY754188	667	14	87.5	751	5	BQ209397	BQ209397	UI-R-DY1-
595	14	87.5	684	9	CE210238	CE210238	668	14	87.5	751	7	CO568111	CO568111	AGENCOURT
596	14	87.5	684	9	CE255791	CE255791	669	14	87.5	752	6	CA312509	CA312509	UI-M-FW0-
597	14	87.5	686	4	BM078495	BM078495	670	14	87.5	758	7	CF952237	CF952237	UI-M-HL0-
598	14	87.5	687	6	CB454191	CB454191	671	14	87.5	758	8	B2096470	B2096470	CH230-236
599	14	87.5	687	7	CO597351	CO597351	672	14	87.5	757	5	BQ205282	BQ205282	UI-R-D21-
600	14	87.5	688	7	CO684084	DG11-1780	673	14	87.5	767	6	CB572909	CB572909	AGENCOURT
601	14	87.5	688	8	BQ263553	BQ263553	674	14	87.5	771	4	BF969066	BF969066	602270001
602	14	87.5	696	4	BY753761	BY753761	675	14	87.5	772	6	CB238171	CB238171	AGENCOURT
603	14	87.5	696	4	BG435548	BG435548	676	14	87.5	776	6	BG923868	BG923868	602824516
604	14	87.5	696	8	BY762798	BY762798	677	14	87.5	777	4	BG245752	BG245752	602358543
605	14	87.5	696	8	AQ380435	RPCI11-16	678	14	87.5	778	8	BO5083	BO5083	CSRL-54D3-u
606	14	87.5	697	4	BI753342	BI753342	679	14	87.5	778	9	CE233274	CE233274	l1gr-g88-
607	14	87.5	697	6	CA422848	UI-H-PE1-	680	14	87.5	779	7	CN458776	CN458776	UI-M-HB0-
608	14	87.5	697	6	CA431599	UI-H-FG1-	681	14	87.5	782	4	BG976173	BG976173	602846407

C 682	14	87.5	785	5	BU938811	AGENCOURT	C 755	14	87.5	914	7	CK160279	FGAS04184
683	14	87.5	785	5	AG305561	Mue muerchu	756	14	87.5	917	5	BO710323	AGENCOURT
684	14	87.5	785	2	BE267052	HV CEA001	C 757	14	87.5	918	5	CL481394	SAITL 340
685	14	87.5	787	2	BR496165	AT09894.5	C 758	14	87.5	919	5	BK456183	EX456183
686	14	87.5	788	2	BF506017	AT08366.5	C 759	14	87.5	921	4	BG754328	BG754328
C 687	14	87.5	788	4	BT760288	603045353	C 760	14	87.5	921	5	BO711247	AGENCOURT
C 688	14	87.5	790	4	BG847553	1024017H1	C 761	14	87.5	921	7	CF582656	AGENCOURT
C 689	14	87.5	793	6	CB602173	AGENCOURT	C 762	14	87.5	925	6	CD359022	AGENCOURT
C 690	14	87.5	798	7	CK476826	AGENCOURT	C 763	14	87.5	926	4	BG761406	AGENCOURT
691	14	87.5	803	5	BU561785	AGENCOURT	C 764	14	87.5	927	8	CC405087	AGENCOURT
692	14	87.5	808	9	BX180023	Dario fer	C 765	14	87.5	927	9	CL027706	CH216-26H
C 693	14	87.5	809	1	AU079824	AU079824	C 766	14	87.5	928	9	CG316604	OSMB66TV
C 694	14	87.5	809	5	AX102623	BX102623	C 767	14	87.5	928	9	CL061017	CH216-93P
695	14	87.5	810	2	CR135688	Reverse B	C 768	14	87.5	929	4	B1558719	603241436
C 696	14	87.5	811	2	BE382952	601298937	C 769	14	87.5	933	9	CG264081	OC00622TH
C 697	14	87.5	821	7	CK478486	AGENCOURT	C 770	14	87.5	936	5	BQ228431	AGENCOURT
698	14	87.5	821	6	CA473760	AGENCOURT	C 771	14	87.5	937	5	CNS05KCC	AGENCOURT
699	14	87.5	823	7	CK198465	FGAS00695	C 772	14	87.5	942	5	BO712604	AGENCOURT
C 700	14	87.5	830	4	BI454760	DIOBOPH11	C 773	14	87.5	942	5	BU150688	AGENCOURT
701	14	87.5	831	6	CA194529	SCVPS1106	C 774	14	87.5	947	5	BO918897	AGENCOURT
702	14	87.5	832	2	BR383361	602045022	C 775	14	87.5	947	5	BU859623	AGENCOURT
703	14	87.5	832	4	BG117202	602346481	C 776	14	87.5	949	9	CG270680	OC1DM337H
C 704	14	87.5	837	5	BO710702	AGENCOURT	C 777	14	87.5	951	4	BG172230	602333373
705	14	87.5	838	2	BF256481	HVMEB001	C 778	14	87.5	954	2	BE213711	HV CEB000
706	14	87.5	839	2	BO889770	AGENCOURT	C 779	14	87.5	958	2	BF793052	602254022
C 707	14	87.5	840	7	CF932841	TREB-T-B04	C 780	14	87.5	962	4	B1692831	603343132
C 708	14	87.5	842	9	CC532607	CH240.410	C 781	14	87.5	970	9	CNS057R2	Tetradon
709	14	87.5	845	4	BI409569	602963988	C 782	14	87.5	972	1	AL542558	AL542558
710	14	87.5	847	6	CB988872	AGENCOURT	C 783	14	87.5	972	5	CG044755	PURCO541B
C 711	14	87.5	847	6	CK196957	FGAS00542	C 784	14	87.5	975	9	CNS05SRA	Tetradon
C 712	14	87.5	851	7	CA466806	AGENCOURT	C 785	14	87.5	977	9	CG264088	OG00622TV
C 713	14	87.5	851	6	CG044757	PURCO541D	C 786	14	87.5	978	2	BE531316	601235425
C 714	14	87.5	854	7	CF551150	AGENCOURT	C 787	14	87.5	979	9	CL031650	CH216-33C
C 715	14	87.5	854	7	BO889871	AGENCOURT	C 788	14	87.5	982	9	CNS05T4E	Tetradon
716	14	87.5	859	8	BZ570391	MBH2_1348	C 789	14	87.5	986	2	BE728764	601564451
C 717	14	87.5	861	3	AY103911	Zee mays	C 790	14	87.5	989	4	BI410801	602963585
718	14	87.5	861	3	CG708030	OGUGR87H	C 791	14	87.5	990	5	BO708919	AGENCOURT
719	14	87.5	862	4	BG321590	D801_01a0	C 792	14	87.5	991	9	CNS05FPA2	Tetradon
C 720	14	87.5	863	1	AU133377	AU133377	C 793	14	87.5	995	4	BI558564	602400563
721	14	87.5	866	6	CD358424	AGENCOURT	C 794	14	87.5	995	4	CA1209275	SCRZAD1C0
722	14	87.5	866	6	CO557901	AGENCOURT	C 795	14	87.5	1005	6	CA148958	SCULR2102
C 723	14	87.5	867	8	AQ750212	HS_5576_A	C 796	14	87.5	1007	6	AO090745	AGU90745
C 724	14	87.5	871	5	BU423977	603955689	C 797	14	87.5	1012	1	EC4543266	Eguae cab
C 725	14	87.5	871	9	CL102463	ISH1-40B2	C 798	14	87.5	1012	9	CNS05GXP	Tetradon
C 726	14	87.5	872	4	BG111391	602281756	C 799	14	87.5	1019	5	BU520311	AGENCOURT
727	14	87.5	872	4	BI691366	603309685	C 800	14	87.5	1020	5	BO715228	AGENCOURT
728	14	87.5	872	4	CK158553	FGAS03982	C 801	14	87.5	1030	1	AL557316	AL557316
729	14	87.5	876	9	CC708043	OGUGR87TV	C 802	14	87.5	1033	9	CNS05SKT	Tetradon
C 730	14	87.5	879	7	CK159831	FGAS04134	C 803	14	87.5	1034	6	CA248169	SCCCPL509
C 731	14	87.5	881	7	CK156540	FGAS03753	C 804	14	87.5	1036	9	CA548169	SCCCPL509
C 732	14	87.5	882	7	CK160000	FGAS04153	C 805	14	87.5	1039	9	CL258403	CA789164
C 733	14	87.5	883	7	CK159412	FGAS04085	C 806	14	87.5	1045	6	CA789164	CA789164
C 734	14	87.5	885	2	BU141397	601135996	C 807	14	87.5	1052	9	CNS035VP	AGENCOURT
C 735	14	87.5	886	2	BP185840	601817547	C 808	14	87.5	1052	9	CNS05BHR	AGENCOURT
C 736	14	87.5	887	5	BO710980	AGENCOURT	C 809	14	87.5	1052	9	CNS05LIP	AGENCOURT
737	14	87.5	888	4	BM045557	603623701	C 810	14	87.5	1054	9	CNS05LTF	AGENCOURT
C 738	14	87.5	893	7	CNS03288	AGENCOURT	C 811	14	87.5	1070	9	CNS05T4F	AGENCOURT
C 739	14	87.5	894	4	BI409472	602961837	C 812	14	87.5	1076	9	CNS04VKT	AGENCOURT
C 740	14	87.5	895	8	CC412230	PURHC42TD	C 813	14	87.5	1076	9	CNS05124	AGENCOURT
741	14	87.5	896	9	CNS04WFB	Tetradon	C 814	14	87.5	1078	8	BZ559798	pac682-164
C 742	14	87.5	897	9	CR797873	GR0AA16C	C 815	14	87.5	1082	9	CNS05R0X	AGENCOURT
C 743	14	87.5	898	9	CK161092	FGAS04276	C 816	14	87.5	1084	9	CNS05C16	Tetradon
744	14	87.5	898	4	CNS05MCO	Tetradon	C 817	14	87.5	1088	8	CC224467	CH261-41N
745	14	87.5	899	4	BI415002	602991088	C 818	14	87.5	1089	9	CNS05EKS	AGENCOURT
C 746	14	87.5	899	4	CK160354	FGAS04192	C 819	14	87.5	1094	7	CE837772	AGENCOURT
C 747	14	87.5	900	7	CK160334	FGAS04190	C 820	14	87.5	1094	9	CNS05CDX	AGENCOURT
C 748	14	87.5	902	7	CR224767	Forward B	C 821	14	87.5	1097	9	CNS05000	Tetradon
C 749	14	87.5	906	4	BO928686	AGENCOURT	C 822	14	87.5	1101	9	CNS051PW	Tetradon
750	14	87.5	907	4	BI956538	HVMEB000	C 823	14	87.5	1101	9	CNS056VE	AGENCOURT
C 751	14	87.5	907	4	BO231653	AGENCOURT	C 824	14	87.5	1101	9	AL323961	Tetradon
C 752	14	87.5	910	1	AL536370	AGENCOURT	C 825	14	87.5	1101	9	AL324821	Tetradon
C 753	14	87.5	910	7	CK160456	FGAS04204	C 826	14	87.5	1101	9	CNS059ZN	Tetradon
C 754	14	87.5	910	7	CK160456	FGAS04204	C 827	14	87.5	1101	9	AL327884	Tetradon

828	14	87.5	1101	9	CNS05T54	AI352705	Tetradon	C 901	13	81.2	215	1	AI565875
829	14	87.5	1106	5	BM801035	BM801035	AGENCOURT	C 902	13	81.2	215	2	BF833898
C 830	14	87.5	1110	5	BQ963301	BQ963301	AGENCOURT	C 903	13	81.2	215	4	BG842275
831	14	87.5	1121	4	B1730441	B1730441	CG0350765	C 904	13	81.2	215	4	BM447515
832	14	87.5	1123	7	CK162021	CK162021	FGAS01460	C 905	13	81.2	215	8	AZ090935
C 833	14	87.5	1123	7	CK208379	CK208379	FGAS02009	C 906	13	81.2	215	8	AZ097539
C 834	14	87.5	1127	4	BM558565	BM558565	AGENCOURT	C 907	13	81.2	217	8	AZ779530
C 835	14	87.5	1129	8	CC240740	CC240740	CH261-45B	C 908	13	81.2	218	2	BB467859
836	14	87.5	1156	9	CNS05178	AI316496	Tetradon	C 909	13	81.2	218	6	CA507975
837	14	87.5	1156	4	BM556141	BM556141	AGENCOURT	C 910	13	81.2	218	9	CL209333
838	14	87.5	1164	5	BM908805	BM908805	AGENCOURT	C 911	13	81.2	219	2	BE767980
C 839	14	87.5	1201	9	CNS04VPC	AI309909	Tetradon	C 912	13	81.2	222	9	CE598153
840	14	87.5	1261	5	BQ059904	BQ059904	AGENCOURT	C 913	13	81.2	223	4	BG315747
841	14	87.5	1321	4	BG684874	BG684874	G02636608	C 914	13	81.2	223	9	AG588108
842	14	87.5	1354	4	CNS0A5YO	BX823295	Arabidops	C 915	13	81.2	223	9	CE487126
843	14	87.5	1377	3	CNS0A5BP	BX823295	Arabidops	C 916	13	81.2	224	1	AL731948
844	14	87.5	1412	3	CNS0A5FP	AK075586	Mus muscu	C 917	13	81.2	224	9	CE290517
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C 846	14	87.5	1754	9	AY412901	AY412901	Mus muscu	C 919	13	81.2	227	4	BG687885
847	14	87.5	2508	9	AY412901	AK046259	Mus muscu	C 920	13	81.2	229	9	CE556670
848	14	87.5	2928	3	AK046259	AI110229	Homo sapi	C 921	13	81.2	230	1	AV258891
849	14	87.5	3474	3	HSMB00886	AK039769	Mus muscu	C 922	13	81.2	230	5	BO818744
C 850	14	87.5	3721	3	AK039769	AK080967	Mus muscu	C 923	13	81.2	230	9	CE038670
C 851	14	87.5	4123	3	AK080967	AL3390128	Homo sapi	C 924	13	81.2	231	2	BB300495
C 852	14	87.5	4828	3	HSMB02759	AK7991730	BM0041F14	C 925	13	81.2	232	1	AV017466
853	13	81.2	107	8	AZ791730	BX611415	BM611415	C 926	13	81.2	232	2	BB838317
854	13	81.2	111	5	BX611415	AL659777	AL659777	C 927	13	81.2	234	1	AV058652
855	13	81.2	114	1	AL659777	CY150165	MDc1r3074	C 928	13	81.2	234	4	AV332448
856	13	81.2	115	7	CV150165	CN636852	139H11_54	C 929	13	81.2	235	4	BI125577
857	13	81.2	117	7	CN636852	BU927050	sa695a10.	C 930	13	81.2	235	9	CE033183
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C 859	13	81.2	120	2	BE934180	CK925050	CFEmcg_01	C 932	13	81.2	236	1	AI841550
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C 862	13	81.2	145	1	AA426123	AA426123	zv52e11.8	C 935	13	81.2	238	2	BB075507
863	13	81.2	150	2	AA387643	BE171187	QV3-HT054	C 936	13	81.2	239	4	BI004928
C 864	13	81.2	152	2	BE171187	B2767989	SALC_1396	C 937	13	81.2	240	1	AA072881
C 865	13	81.2	152	8	B2767989	AI1842824	UI-M-A01-	C 938	13	81.2	240	1	AA072881
866	13	81.2	155	5	BI048926	BO149076	NEP087809F	C 939	13	81.2	240	5	BX635692
867	13	81.2	155	8	BI048926	AO005378	CIT-HSP-2	C 940	13	81.2	242	6	CB863441
868	13	81.2	159	8	AO005378	AI938864	sc61h06.Y	C 941	13	81.2	244	1	AA873831
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C 871	13	81.2	164	6	CB118781	CB024217	NKRV_037	C 944	13	81.2	246	8	AZ236381
872	13	81.2	164	6	CB118781	AM87628	MRI-ST011	C 945	13	81.2	247	1	AA706454
C 873	13	81.2	164	6	CD024217	CE074253	LiGr-G88-	C 946	13	81.2	247	8	BM841897
C 874	13	81.2	177	9	CE074253	CL433016	ZMMBBD044	C 947	13	81.2	248	1	AA831160
C 875	13	81.2	180	2	BE155402	BE155402	PML-HT035	C 948	13	81.2	248	4	BI040623
C 876	13	81.2	182	9	CL872795	BR115302	7H81a11.X	C 949	13	81.2	250	1	AV159888
C 877	13	81.2	182	9	CL872795	AI893438	mt09h06.x	C 950	13	81.2	250	2	AV159888
C 878	13	81.2	184	2	BF15302	BF733981	PM2-ANNO9	C 951	13	81.2	251	1	AV348287
C 879	13	81.2	185	1	AI893438	BB248888	BB248888	C 952	13	81.2	251	9	CE334277
C 880	13	81.2	190	2	BF733981	BI424499	gah50h07.	C 953	13	81.2	252	2	AA462181
881	13	81.2	193	4	BI424499	T36206	EST98455.Hu	C 954	13	81.2	252	7	T99612
C 882	13	81.2	193	4	BI424499	BF989513	CM1-WT018	C 955	13	81.2	254	1	AA226343
C 883	13	81.2	196	2	BF989513	AA163401	me71b09.r	C 956	13	81.2	254	1	AA226343
884	13	81.2	201	1	AV104583	AM865307	PM4-SNN02	C 957	13	81.2	254	7	CF804443
C 885	13	81.2	201	1	AV104583	BE207073	ba09h10.Y	C 958	13	81.2	254	7	CF804443
C 886	13	81.2	203	2	BE207073	CO133140	EST827811	C 959	13	81.2	254	6	CD037605
C 887	13	81.2	205	9	CG567530	CG567530	OST193949	C 960	13	81.2	259	9	CR033529
C 888	13	81.2	205	9	CG567530	AV003495	AV003495	C 961	13	81.2	260	1	AA077298
C 889	13	81.2	209	9	CG605628	CG605628	OST282556	C 962	13	81.2	261	4	BM093980
C 890	13	81.2	211	1	AV243769	AV243769	AV243769	C 963	13	81.2	264	4	BM093980
C 891	13	81.2	211	1	AV243769	AV282192	AV282192	C 964	13	81.2	267	4	BM818153
C 892	13	81.2	212	8	AO288523	AO288523	rbdb0033C	C 965	13	81.2	268	2	AM012658
C 893	13	81.2	213	1	AI845009	AA352555	EST60648	C 966	13	81.2	268	2	AM012658
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C 895	13	81.2	214	6	CD271311			C 968	13	81.2	269	2	BB318197
C 896	13	81.2	214	6	CD271311			C 969	13	81.2	269	2	BB318197
C 897	13	81.2	214	6	CD271311			C 970	13	81.2	269	2	BB318197
C 898	13	81.2	214	6	CD271311			C 971	13	81.2	269	2	BB318197
C 899	13	81.2	214	6	CD271311			C 972	13	81.2	269	2	BB318197
900	13	81.2	214	6	CD271311			C 973	13	81.2	269	2	BB318197

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
BF327943	BF327943	384 bp	MRNA	linear	EST 22-NOV-2000							
LOCUS	BF327943	384 bp	MRNA	linear	EST 22-NOV-2000							
DEFINITION	QV0-BN0148-070700-293-a12 BN0148 Homo sapiens cDNA, mRNA sequence.											
VERSION	BF327943.1	GI:11298691										
KEYWORDS	EST.											
SOURCE	Homo sapiens (human)											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.											
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.											
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed											
JOURNAL	sequence tags											
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)											
PUBMED	20202663											
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&t2=QV0-BN0148-070700-293-a12&t3=2000-07-07&t4=1) Seq primer: puc 18 forward High quality sequence start: 41 High quality sequence stop: 382. Location/Qualifiers 1. .384 /organism="Homo sapiens"											

ALIGNMENTS

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
BF327943	BF327943	384 bp	MRNA	linear	EST 22-NOV-2000							
LOCUS	BF327943	384 bp	MRNA	linear	EST 22-NOV-2000							
DEFINITION	QV0-BN0148-070700-293-a12 BN0148 Homo sapiens cDNA, mRNA sequence.											
VERSION	BF327943.1	GI:11298691										
KEYWORDS	EST.											
SOURCE	Homo sapiens (human)											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.											
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.											
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed											
JOURNAL	sequence tags											
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)											
PUBMED	20202663											
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-GN0295-020101-655-a07&t3=2001-01-02&t4=1) Seq primer: puc 18 forward High quality sequence start: 18 High quality sequence stop: 396. Location/Qualifiers 1. .396 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="GN0295" /note="Organ: Placenta normal; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."											

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
Db 16 AAAGCCACCCAGGCA 31

RESULT 2
BI049449 396 bp MRNA linear EST 15-JUN-2001
CM2-GN0295-020101-655-a07 GN0295 Homo sapiens cDNA, mRNA sequence.
BI049449
BI049449.1 GI:114456979

ALIGNMENTS

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
BF327943	BF327943	384 bp	MRNA	linear	EST 22-NOV-2000							
LOCUS	BF327943	384 bp	MRNA	linear	EST 22-NOV-2000							
DEFINITION	QV0-BN0148-070700-293-a12 BN0148 Homo sapiens cDNA, mRNA sequence.											
VERSION	BF327943.1	GI:11298691										
KEYWORDS	EST.											
SOURCE	Homo sapiens (human)											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.											
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.											
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed											
JOURNAL	sequence tags											
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)											
PUBMED	20202663											
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-GN0295-020101-655-a07&t3=2001-01-02&t4=1) Seq primer: puc 18 forward High quality sequence start: 18 High quality sequence stop: 396. Location/Qualifiers 1. .396 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="GN0295" /note="Organ: Placenta normal; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."											

FEATURES

source
1. .384
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/db_xref="taxon:9606"
/dev_stage="Adult"
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/note="Organ: Placenta normal; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were

ORIGIN performed under low stringency conditions."

Query Match 100.0%; Score 16; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
148 AAAGCCACCCAGGCA 163

RESULT 3
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LOCUS tigr-gss-dog-17000333941473 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
CE327035
VERSION CE327035.1 GI:36139166
KEYWORDS GSS.
SOURCE
ORGANISM Canis familiaris (dog)

Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 441)
Kirchness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
Contact: Kirchness EF
Department of Genomic Research
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirchness@tigr.org
Class: shotgun.

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PubMed
COMMENT

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BclXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
73 AAAGCCACCCAGGCA 88

RESULT 4
AA103554 464 bp mRNA linear EST 29-OCT-1996
LOCUS m024h10.r1 life Tech mouse embryo 13 5dpc 10666014 Mus musculus
DEFINITION cDNA clone IMAGE:554563 5', mRNA sequence.
AA103554
VERSION AA103554.1 GI:1649714
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 464)

AUTHORS

Maria M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT

The WashU-HM Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HM Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:335355
Putative full length read
vector to vector length is 510
Seq primer: -28M13 rev1 from Amersham.

FEATURES
source
Location/Qualifiers
1..464
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/db_xref="taxon:10090"
/clone_lib="IMAGE:554563"
/tissue_type="embryo"
/dev_stage="13.5dpc embryos"
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/clone_lib="Life Tech mouse embryo 13 5dpc 10666014"
/note="Organ: whole embryo; Vector: PCMV-SPORT2; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 13.5dpc embryos. PCMV-SPORT2 vector."

ORIGIN

Query Match 100.0%; Score 16; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
275 AAAGCCACCCAGGCA 260

RESULT 5
BE144757 496 bp mRNA linear EST 21-JUN-2000
LOCUS CM0-HT0180-041099-065-c06 HT0180 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE144757
ACCESSION BE144757
VERSION BE144757.1 GI:8607481
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 496)
Nagai,M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE
JOURNAL
MEDLINE
PubMed
COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/PCR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-CM0-HT0180-041
 099-065-06&t3=1999-10-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 496.

FEATURES

Source

Location/Qualifiers
 1..496
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="HT0180"

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
 |||||
 Db 229 AAAGCCACCCAGGCA 244

RESULT 6

LOCUS

CF755881 587 bp mRNA linear EST 17-OCT-2003

DEFINITION

DSAF1.2 A12.b1 A011 Drought-stressed after flowering Sorghum
 bicolor cDNA clone DSAF1.2_A12_A011 5', mRNA sequence.

ACCESSION

CF755881

VERSION

CF755881.1 GI:37704961

KEYWORDS

EST.

SOURCE

Sorghum bicolor (sorghum)

ORGANISM

Sorghum bicolor (Eurycotyaceae; Strepocophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 587)
 Cordanier-Pratt, M.-M., Zhang, D., McCartor, K., Nguyen, H.T. and
 Pratt, L.H.

AUTHORS

An EST Database from Sorghum: Subtracted post-flowering drought
 stressed leaf tissues

TITLE

Unpublished (2003)

JOURNAL

Contact: Cordanier-Pratt MM

COMMENT

Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@uga.edu

Library constructed at Texas Tech University by Denshi Zhang and
 Jianhang Jia in the laboratory of Dr. Henry Nguyen. Sequencing was
 done in the laboratory for Genomics and Bioinformatics, University
 of Georgia. Sequence data have been trimmed to exclude vector and
 regions below phred quality 16. Three-prime sequences are presented
 as their reverse complement and have been trimmed to exclude polyA.
 Seq primer: JENREV (CAGGAACGCTATGAC).

FEATURES

Source

Location/Qualifiers
 1..587
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="B35"
 /db_xref="taxon:4558"

ORIGIN

/clone="DSAF1.2 A12 A011"
 /dev_stage="Post-flowering"
 /lab_host="Electromax DH10B (BRL)"
 /clone_lib="Drought-stressed after flowering"
 /note="Organ: Leaf; Vector: pBluescriptSK-; Site 1: XhoI;
 Site 2: EcoRI; The library was prepared from polyA+ RNA
 from leaves harvested from post-flowering,
 drought-stressed Sorghum bicolor, cv. B35. Double-stranded
 cDNA was cloned unidirectionally using the Unizap system
 from Stratagene. After amplification, the library was
 subtracted by re-association hybridization. Inserts can be
 excised with XhoI and EcoRI."

Query Match 100.0%; Score 16; DB 7; Length 587;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
 |||||
 Db 225 AAAGCCACCCAGGCA 240

RESULT 7

LOCUS

BQ385327/c 623 bp mRNA linear EST 22-MAY-2002

DEFINITION

NTSC.mn11f10.y1 NICHD_XGC_Ov1 Xenopus laevis cDNA clone
 IMAGE:5073186 5', mRNA sequence.

ACCESSION

BQ385327

VERSION

BQ385327.1 GI:21073014

KEYWORDS

EST.

SOURCE

Xenopus laevis (African clawed frog)

ORGANISM

Xenopus laevis (Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Xenopus.

REFERENCE

1 (bases 1 to 623)
 NIH-XGC http://image.llnl.gov/image/html/xenopus1b.info.shtml.

AUTHORS

National Institute of Child Health and Human Development, National
 Cancer Institute, Xenopus Gene Collection

TITLE

Unpublished (2002)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgabbs-remail.nih.gov

cDNA Library Preparation:
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL.

DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 info@image.llnl.gov

Plate: LLAM1196 row: L column: 19

Seq primer: M13RPI reverse primer (ABT).

FEATURES

Source

Location/Qualifiers
 1..623
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:5073186"
 /sex="female"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD_XGC_Ov1"
 /note="Organ: ovary; Vector: PCMV-SFOR6; Site 1: NciI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.0 kb. Constructed by Life
 Technologies."

ORIGIN

Query Match 100.0%; Score 16; DB 5; Length 623;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGCCACCCAGGCA 16
 |||||

```

Db          519  AAGGCACCAAGCA  504

RESULT  8
LOCUS   CA192813
DEFINITION  SCSLSB1042G03.g SBI Saccharum officinarum cDNA clone SCSLSB1042G03
ACCESSION  CA192813
VERSION   CA192813.1 GI:35139355
KEYWORDS  EST.
SOURCE    Saccharum officinarum
          Saccharum officinarum
          Bukarjota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
          complex.
REFERENCE  1 (bases 1 to 646)
          Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
          The libraries that made SUCEST
          Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Contact: Arruda P
          Centro de Biologia Molecular e Engenhariaia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parreda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bcccenter.fcav.uneep.br
          Plate: 042 row: G column: 03
          Seq primer: T7 Promoter Primer.
FEATURES
     source
         1..646
             /organism="Saccharum officinarum"
             /mol_type="mRNA"
             /db_xref="taxon:4547"
             /clone="SCSLB1042G03"
             /lab_host="DH10B"
             /clone_1lb="SBI"
             /note="Organ: Stalk Bark from adult plants; Vector:
             pSport1; Site_1: SalI; Site_2: NotI; An unidirectional
             cDNA library generated from [Stalk Bark from adult
             plants]. cDNA was prepared from polyA+ mRNA using
             Superscript Plasmid System Kit (Invitrogen). The
             super-8-strand cDNAs were fractionated in a agarose
             CL-2B 40cm-columns and fragments sizing between 0.8 and
             1.5 Kb were directionally cloned into the vector. Details
             of each source of RNA and library construction can be
             obtained at http://succest.fad.unicamp.br/public"

ORIGIN
Query Match      100.0%; Score 16; DB 6; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1  AAGGCACCAAGCA  16
      |||||||||||||
Db      63  AAGGCACCAAGCA  78

RESULT  9
LOCUS   BBS45848/c
DEFINITION  BBS45848 RIKEN full-length enriched, 0 day neonate eyeball Mus
ACCESSION  BBS45848
VERSION   BBS45848.2 GI:16447378
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
          Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE	TITLE
AUTHORS	JOURNAL
COMMENT	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 659)	
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiamoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komoto,H., Koyda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)	
On Jul 31, 2000 this sequence version replaced gi:9617276. Unpublished (2001)	
Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216	
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komoto,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)	
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)	
Komoto,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanae,T., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)	
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
Location/Qualifiers	
1. 659	
/organism="Mus musculus"	
/mol_type="mRNA"	
/db_xref="taxon:10090"	
/cfeature="E130306004"	
/clone_type="eyeball"	
/dev_stage="0 day neonate"	
/lab_host="DH10B"	
/clone_id="RIKEN full-length enriched, 0 day neonate eyeball"	
/note="Site_1: Sali; Site_2: Banfi; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAAGAGAGAGCGCGCCGACCTCGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGAGAGTTCTCGAGTTCTAATTAATTCATCCCCCCCC 3']. cDNA	

was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCACCAAGCA 16
|||||
DB 434 AAAGCACCACCAAGCA 419

RESULT 10 666 bp mRNA linear EST 23-SEP-2003
CA083440
LOCUS SCEPAM013G09.g AM2 Saccharum officinarum cDNA clone SCEPAM013G09
DEFINITION
5', mRNA sequence.
CA083440
VERSION CA083440.1 GI:34936751
KEYWORDS
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

REFERENCE 1 (bases 1 to 666)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcap.unesp.br
Plate: 013 row: G column: 09
Seq primer: T7 Promoter Primer.

FEATURES

source

Location/Qualifiers
1..666
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEPAM013G09"
/lab_host="DH10B"
/clone_id="AM2"
/note="Organ: Apical meristem and tissues surrounding of
immature plants; Vector: pSport1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[Apical meristem and tissues surrounding of immature
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCACCACCAAGCA 16
|||||
DB 471 AAAGCACCACCAAGCA 486

RESULT 11
AV359761/c

LOCUS AV359761

DEFINITION AV359761 RIKEN full-length enriched, adult male eyeball Mus

musculus cDNA clone 7530401G06 3', mRNA sequence.

ACCESSION AV359761

VERSION AV359761.2 GI:16397410

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 700)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Kono,M., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Nov 13, 1999 this sequence version replaced gi:6406899.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9226
Email: genome-resesc.riken.jp, URL:<http://genome.gsc.riken.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

source

Location/Qualifiers
1..700
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7530401G06"
/sex="male"
/tissue_type="eyeball"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="RIKEN full-length enriched, adult male
eyeball"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTAAATTAATCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"

ORIGIN

Query Match 100.0%; Score 16; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
|||||
Db 110 AAAGCCACCCAGGCA 95

RESULT 12
CD778583/c 770 bp mRNA linear EST 01-JUL-2004
LOCUS EST649944 RAA Rhipicephalus appendiculatus cDNA clone RAA309 3'
DEFINITION end, mRNA sequence.

ACCESSION CD778583
VERSION CD778583.1 GI:49534256
KEYWORDS EST.
SOURCE Rhipicephalus appendiculatus
ORGANISM Rhipicephalus appendiculatus

REFERENCE Eukaryote, Metazoa, Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
1 (bases 1 to 770)
Nene, V., Lee, Y., Skilton, R., Mwaura, S., Quackenbush, J., Gardner, M. and Bishop, R.

TITLE An index of genes transcribed in the salivary glands of Rhipicephalus appendiculatus
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST649945
Contact: Vithvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@igf.org

FEATURES
Source
1. .770
Location/Qualifiers
/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RAA309"
/dev_stage="Adult"
/lab_host="B. coli strain DH10B-Tona"
/clone_id="RAA"
/note="Organ: Salivary glands; Vector: pCMVSPORT6.0.cdb;
Salivary glands were dissected on day four after
initiation of feeding. Total RNA was prepared using acid
guanidium thiocyanate-phenol-chloroform extraction. The
cDNA library was custom prepared by Invitrogen
Corporation. Briefly, first strand cDNA was primed using
oligo(dT) containing a NotI site. Size fractionated double

stranded cDNA was ligated to EcoRV-NotI cleaved vector and electroporated into E.coli. Library RAA was made from uninfected ticks."

ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
|||||
Db 257 AAAGCCACCCAGGCA 242

RESULT 13
BI250824 895 bp mRNA linear EST 17-JUL-2001
LOCUS 602993448F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149306 5'
DEFINITION mRNA sequence.

ACCESSION BI250824
VERSION BI250824.1 GI:14799568
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 895)
NIH-MGC http://mgc.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
UNPUBLISHED (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLU at:
http://image.lnl.gov
Plate: LLM1368 row: p column: 11
High quality sequence start: 4
High quality sequence stop: 741.
Location/Qualifiers

FEATURES

1. .895
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5149306"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_id="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 100.0%; Score 16; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGCCACCCAGGCA 16
|||||
Db 2 AAAGCCACCCAGGCA 17

RESULT 14
CA474404/c 975 bp mRNA linear EST 12-NOV-2002
LOCUS CA474404
DEFINITION AGENCOURT_10667749 NCI_CGAP_ZK1d1 Danio rerio cDNA clone

IMAGE:6795444 5', mRNA sequence.
 ACCESSION CA474404
 VERSION CA474404.1 GI:24930756
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 975)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Leonard I. Zon, M.D.
 CDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
 Plate: LLM4305 row: 1 column: 11
 High quality sequence stop: 314.
 Location/Qualifiers
 1..975
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:6795444"
 /lab_host="DH10B (T1-resistant)"
 /note="Organ: kidney; Vector: PCW-Sports.1; site: 1; EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI CGAP library."

ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 975;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 Db 621 AAAGCCACCCAGGCA 606

RESULT 15
 W34362/c
 LOCUS
 DEFINITION 987 bp mRNA linear EST 11-SEP-1996
 IMAGE:31815 5', similar to SM:KELC_DROME O04652 RING CANAL PROTEIN
 ; mRNA sequence.
 W34362
 W34362.1 GI:1316273
 EST.
 Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 987)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Scheilenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Teising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 CONTACT: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:209431
 Seq primer: Eppimer
 High quality sequence stop: 363.
 Location/Qualifiers
 1..987
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:31815"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares mouse p3NMF19.5"
 /note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAACTGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

ORIGIN

Query Match 100.0%; Score 16; DB 7; Length 987;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
 |||||
 Db 361 AAAGCCACCCAGGCA 346

RESULT 16
 CG754259/c
 LOCUS
 DEFINITION 1684 bp DNA linear GSS 24-OCT-2003
 P049-3-E10-Ya Ppa EcoRI BAC library Pristionchus pacificus genomic,
 genomic survey sequence.
 CG754259
 CG754259.1 GI:37979569
 GSS.
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 1 (bases 1 to 1684)
 Srinivasan, J., Sins, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
 An integrated physical and genetic map of the nematode Pristionchus pacificus
 Mol. Genet. Genomics 269 (5), 715-722 (2003)
 22835951
 12884007
 CONTACT: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 Class: BAC ends.
 Location/Qualifiers
 1..1684
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"

FEATURES
 source

ORIGIN

/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

Query Match 100.0%; Score 16; DB 9; Length 1684;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||||
1224 AAAGCCACCCAGGCA 1209

RESULT 17
AK009491/c
LOCUS 2005 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310024D23 product:CDNA FLJ32015 FIS, CLONE
NTN0N1000052, WEAKLY SIMILAR TO RATTUS NORVEGICUS KEXCH RELATED
PROTEIN 1 homolog [Homo sapiens], full insert sequence.

ACCESSION AK009491 GI:12844320
VERSION AK009491.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636

2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PubMed 11042159

3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Iehli, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PubMed 11076861

4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861
PubMed 11076861

5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 120530913
PubMed 11076861

6
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Imotani, K., Iehli, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komno, H., Kouda, M.,
Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Noma, S., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shitaki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
details.

COMMENT

FEATURES

source

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3']. cDNA was
prepared by using trihalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. Second
strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGCTTATTAAATTATNCCCCCCCCCCC 3']. cDNA was cleaved
with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

Location/Qualifiers

1. 2005
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM:DB:2310024D23"
/db_xref="taxon:10090"
/clone="2310024D23"
/sex="male"
/tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
86. 1951
/note="unnamed protein product; CDNA FLJ32015 FIS, CLONE
NTN0N1000052, WEAKLY SIMILAR TO RATTUS NORVEGICUS KEXCH
RELATED PROTEIN 1 homolog [Homo sapiens] (SPT096MR2,
evidence: PASTY, 91.5%ID, 93.8%length, match=1329)
putative"
/codon_start=1
/protein_id="BAB26321.1"
/db_xref="GI:12844321"
/translation="MTGLGEQAEQQLVYQTLIDGLKMDLHGKRLDVCYRGSEF
PCHRLVLAQSPYFRFRFLAEPSAGVLEEVSPVQVHLVLTSEIALDASVQ
DLEFAAHRFQIPISFTICVSPLOKRLCLNCLAVPFLGLDCLARLAVARDICAF
PLVARNDFLGLSADLELAIISDGLNKEKEAVFANVWMSGGAEOAQRORLP
TVESVRCRLPRAFLERVRHPPLVRSQPELRKQVMDAEGELTLTKRKKEG
EOTARKEANOGEDTKARDDEERYVGLINDLRGMDLQDLMISEGGAAYADA
ANECYASLSIOIPKRVSLVATKENVPPAGGCFYVNDKEDPMASVPLQFDLDEA
LDMPLESPRCFLGELBALNATVVGGRGLKSEDSLDVLTCDRLSFKGESDPLPY
AVYGHVLSHMDLVVITGGKGRKCLNKKCVYDPPKRFMKELAPQVARSICGATVH
DRIIFVAGVDTDLGTVSSSEVSIADNKKTSFPAQPOERSISLVLGATLVMLGFA
TLETSGELVPELNDIWRYNDEKWEQVLEIAVAAGATFLPRLNVRLTKM"

ORIGIN

Query Match 100.0%; Score 16; DB 3; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGCA 16
|||||
Db 1780 AAAGCCACCCAGGCA 1765

RESULT 18
AK078669/c
LOCUS
DEFINITION
AK078669 2368 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male eyeball cDNA, RIKEN full-length enriched library, clone:7530401G06 product:CDNA FLJ32015 FIS, CLONE NTONG1000052, WEAKLY SIMILAR TO RATTUS NORVEGICUS K14CH RELATED PROTEIN 1 homolog (Homo sapiens), full insert sequence.

ACCESSION
AK078669.1 GI:26098028
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
10349636
2
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishii, K., Kitamura, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, U., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1617-1630 (2000)
20499374
11042159
4
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2368)
Aachai, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirose, T., Hirose, T., Horii, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazaki, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, K., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Yamanaka, S., Yamanura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yatsunami, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Science Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES
source
1..2368
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:7530401G06"
/db_xref="taxon:10090"
/clone="7530401G06"
/sex="male"
/tissue_type="eyeball"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
83..1949
/note="CDNA FLJ32015 FIS, CLONE NTONG1000052, WEAKLY SIMILAR TO RATTUS NORVEGICUS K14CH RELATED PROTEIN 1 homolog (Homo sapiens) (SPTK106MR2, evidence: FAST), 91.5%ID, 93.8%length, match=1329)
putative"
2347..2352
/note="putative"
2368
/note="putative"

misc_feature
polya_signal
polya_site
ORIGIN
Query Match 100.0%; Score 16; DB 3; Length 2368;
Best Local Similarity 100.0%; Pred. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 AAAGCCACCACCAAGCA 16
|||||
Db 1778 AAGGCCACCCCAAGCA 1763

RESULT 19
BB198017
LOCUS
DEFINITION
BB198017 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330105M01.3', mRNA sequence.
VERSION
BB198017
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 231)
Komoto, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirose, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koyama, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watanabe, S., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshihide, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Komoto, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Thermosensitization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, U., Shibata, K., Iwata, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.
 Location/Qualifiers
 1. 231
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A330105M01"
 /sex="male"
 /tissue_type="spinal cord"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="RIKEN full-length enriched, adult male spinal cord"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATCCAGACCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCCAGACCTTTTCTTTTCTTTTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from lambda FLC 1."

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAGCACCACCAAGC 15
 |||||
 Db 138 AAAGCACCACCAAGC 152

RESULT 20
 BF924007 268 bp mRNA linear EST 19-JAN-2001
 LOCUS CM2-NT0170-251100-530-h08 NT0170 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF924007
 ACCESSION BF924007.1 GI:12319895
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 268)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPER/PICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t=CM2-NT0170-251100-530-h08&t3=2000-11-25&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 12
 High quality sequence stop: 268.
 Location/Qualifiers
 1. 268
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_1lb="NT0170"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 AAGCACCACCAAGCA 16
 |||||
 Db 84 AAGCACCACCAAGCA 98

RESULT 21
 BB090939 285 bp mRNA linear EST 23-JUN-2000
 LOCUS BB090939 RIKEN full-length enriched, 12 days embryo, embryonic body
 DEFINITION BB090939
 ACCESSION BB090939
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 285)
 Kono, H., Alizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, D., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyoawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Miuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shitaki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Wataniki, A.,

TITLE
JOURNAL
COMMENT
Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagasaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermocycling of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuina, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
source
Location/Qualifiers
1. .285
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9430028f19"
/tissue_type="embryonic body between diaphragm region and neck"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTATTAATTAATTCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI."

ORIGIN
Query Match 93.8%; Score 15; DB 2; Length 285;
Best local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCACCCAGGC 15
Db 197 AAAGCCACCCAGGC 211

RESULT 22
BB309456/c 287 bp mRNA linear EST 10-JUL-2000
LOCUS BB309456 RIKEN full-length enriched, adult male corpora
DEFINITION quadrigenina Mus musculus cDNA clone B230310M21 3' similar to M81342 BALB/c fibroblast growth factor receptor 3 (mfr3) mRNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

BB309456
BB309456.1 GI:9010161
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 287)
Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Wachihi, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagasaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermocycling of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuina, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

Location/Qualifiers
1. .287
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="B230310M21"
/sex="male"
/tissue_type="corpora quadrigenina"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male corpora quadrigenina"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTATTAATTAATTCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a

modified pbluescript KS(+) after bulk excision from lambda
FLC I."

Query Match 93.8%; Score 15; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
Db 169 AAAGCCACCCAGGC 155

RESULT 23
W40391 294 bp mRNA linear EST 20-MAY-1996
LOCUS z80e10.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328650 5'
DEFINITION similar to gb:U13748 EUKARYOTIC INITIATION FACTOR 4A-I (HUMAN);,
mRNA sequence.

ACCESSION W40391 GI:1324172
VERSION W40391.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 294)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Roifling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Warr, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PubMed 8889549

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 243.

FEATURES
source location/Qualifiers

1..294
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1262854"
/db_xref="taxon:9606"
/clone="IMAGE:328650"
/issue_type="pancreatic islet"
/lab_host="SOB cells (kanamycin resistant)"
/clone_lib="Pancreatic Islet"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993)
Takeda et al. Cloned unidirectionally. Primer: Oligo dt.
-5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor
sequence: 5' CTCAGCTTTT TTTT TTTT TTTT 3' "

ORIGIN

Query Match 93.8%; Score 15; DB 7; Length 294;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
Db 209 AAAGCCACCCAGGC 223

RESULT 24

B1036238 306 bp mRNA linear EST 14-JUN-2001
LOCUS CM3-NT0245-030101-599-f10 NT0245 Homo sapiens cDNA, mRNA sequence.
ACCESSION B1036238
VERSION B1036238.1 GI:14442864
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 306)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.P., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPS/P/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM3&t2=CM3-NT0245-
030101-599-f10&t3=2001-01-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 306.

FEATURES
source location/Qualifiers

1..306
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0245"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 93.8%; Score 15; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
Db 113 AAGCCACCCAGGCA 127

RESULT 25

BB251202 310 bp mRNA linear EST 06-JUL-2000
LOCUS BB251202 RIKEN full-length enriched, 7 days neonate cerebellum Mus
DEFINITION musculus cDNA clone A730045D02 3', mRNA sequence.

ACCESSION BB251202
VERSION BB251202.1 GI:8943948
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

JOURNAL Unpublished (1998)
 COMMENT Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org

This clone is available through the ATCC, contact the ATCC
 tel#703-365-2700 for further information
 Seq primer: M13 Reverse.

FEATURES
 Source Location/Qualifiers

1..328
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="RG1086"
 /tissue_type="mix - brain, ovary, placenta, kidney, lung,
 liver, embryo, heart, muscle, spleen"
 /lab_host="SOLR"
 /clone_lib="Rat gene index, normalized rat, norvegicus,
 Bento Soares"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; Estimated insert size approx.1 kb"

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCCACCCAGGC 15
 Db 243 AAGCCACCCAGGC 257

RESULT 28 362 bp mRNA linear EST 22-JAN-2001
 LOCUS IL2-NT0203-271200-322-A10 NT0203 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF935524
 VERSION BF935524.1 GI:12352848
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 362)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 PUBMED 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL2ct2-IL2-NT0203-
 271200-322-A10ct3-2000-12-27ct4e1)
 Seq primer: puc 18 forward
 High quality sequence stop: 324.
 Location/Qualifiers

source

1..362
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0203"
 /note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAGCCACCCAGGCA 16
 Db 184 AAGCCACCCAGGCA 198

RESULT 29 365 bp mRNA linear EST 18-AUG-2004
 LOCUS csa02-2m93-g01 Csa02 Cucumis sativus cDNA clone csa02-2m93-g01 5',
 DEFINITION mRNA sequence.
 ACCESSION CV001930
 VERSION CV001930
 KEYWORDS EST.
 SOURCE Cucumis sativus (cucumber)
 ORGANISM Cucumis sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

1 (bases 1 to 365)
 dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
 Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
 Leebens-Mack, J., Landherr, L., Perl-Treves, R., Ilut, D. and Wall, K.
 Generation of ESTs from early female flower buds of Cucumis sativus
 Unpublished (2003)
 CONTACT: Claude dePamphilis or James Leebens-Mack
 Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
 State University, University Park, PA 16802, USA
 Tel: 814 863 6413
 Fax: 814 865 9131
 Email: cwt3@psu.edu or jh110@psu.edu

The sequence provided is trimmed of vector and low quality regions.
 Full sequence and original trace file are available from the Plant
 Genome Network website (http://pgn.cornell.edu)
 Plate: csa02-2m93 row: 9 column: 01
 Seq primer: M13P.

FEATURES

Source

Location/Qualifiers
 1..365
 /organism="Cucumis sativus"
 /mol_type="mRNA"
 /db_xref="taxon:3659"
 /clone="csa02-2m93-g01"
 /tissue_type="female flower buds"
 /dev_stage="clmm buds"
 /lab_host="SOLR"
 /clone_lib="Csa02"
 /note="Vector: pBluescript SK (+/-); Site_1: EcoRI;
 Site_2: XhoI; This is a directionally cloned,
 non-normalized library. This library has been generated by
 the Floral Genome Project (FGP). The Floral Genome Project
 is funded by NSF's Plant Genome Research Program
 (DBI-0115684). More information about the project can be
 obtained at http://fgp.bio.psu.edu"

ORIGIN

Query Match 93.8%; Score 15; DB 7; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
 Db 239 AAAGCCACCCAGGC 253

RESULT 30

CB691996

LOCUS 375 bp mRNA linear EST 10-APR-2003
 DEFINITION AMGNNUC:SRPG2-00067-E11-A SRPG2 (10238) Rattus norvegicus cDNA
 clone SRPG2-00067-e11 5', mRNA sequence.

ACCESSION CB691996
 VERSION CB691996.1 GI:29749143
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine;

REFERENCE 1 (bases 1 to 375)
 AUTHORS Amgen EST Program.
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00067 row: e column: 11.
 Location/Qualifiers

FEATURES
 source 1..375
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="srpg2-00067-e11"
 /tissue_type="pancreal gland brain"
 /clone_lib="srpg2 (10238)"
 /note="Vector: pSPORT1, Site_1: SalI, Site_2: NotI; pancreal gland brain region"

ORIGIN

Query Match 93.8%; Score 15; DB 6; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
 Db 343 AAAGCCACCCAGGC 357

RESULT 31

CB698527

LOCUS 394 bp DNA linear GSS 29-SEP-2003
 DEFINITION tigr-gss-dog-17000368753766 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION CB698527
 VERSION CB698527.1 GI:37017751
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

Kirkness, E.F., Batna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432

PUBMED

14512627

Contact: Kirkness EF

The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA

Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

source

Location/Qualifiers
 1..394
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 93.8%; Score 15; DB 9; Length 394;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCCAGGC 15
 Db 103 AAAGCCACCCAGGC 89

RESULT 32

CE047936/c

LOCUS 401 bp DNA linear GSS 24-SEP-2003
 DEFINITION tigr-gss-dog-17000357497477 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION CE047936
 VERSION CE047936.1 GI:35087093
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

Kirkness, E.F., Batna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers
 1..401
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

FEATURES

source

ORIGIN

Query Match 93.8%; Score 15; DB 9; Length 401;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGCCACCCAGGCA 16

Db 238 AAGCCACCAAGCA 224

RESULT 33
BIS36031 408 bp mRNA linear EST 30-AUG-2001

LOCUS 30188 MRC 4BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION BIS36031

ACCESSION BIS36031.1 GI:15377141

VERSION EST.

KEYWORDS Bos taurus (cow)

SOURCE Bos taurus

ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 408)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pette,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

PUBMED 11282978

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGATCGACG
Plate: 114 row: C column: 7
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source
1. .408
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from day 20 and day 40 embryos."

ORIGIN

Query Match 93.8%; Score 15; DB 4; Length 408;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 AAGCCACCAAGCA 16
|||||
74 AAGCCACCAAGCA 88

RESULT 34
AA053186 417 bp mRNA linear EST 13-SEP-1996

LOCUS 2172a04.c1 StrataGene colon (#937204) Homo sapiens cDNA clone

DEFINITION IMAGE:510126 5' similar to gb:DJ1748 EUKARYOTIC INITIATION FACTOR 4A-I (HUMAN); mRNA sequence.

ACCESSION AA053186

VERSION AA053186.1 GI:1544395

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 417)

AUTHORS Hillier,L., Lennon,G., Becker,M., Ronaldo,M.F., Chipelli,B., Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Scheilenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 8889549

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 404.

FEATURES
source
1. .417
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3813459"
/db_xref="taxon:9606"
/clone="IMAGE:510126"
/tissue_type="tumor"
/cell_line="T84 carcinoma cell line"
/lab_host="SOLR cells (Kanamycin resistant)"
/clone_lib="StrataGene colon (#937204)"
/note="Organ: colon; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: oligo dT. T-84 colonic epithelial cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

Query Match 93.8%; Score 15; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 AAGCCACCAAGCA 15
|||||
289 AAGCCACCAAGCA 303

RESULT 35
B0198462 419 bp mRNA linear EST 07-MAY-2003

LOCUS NKLV31.B01.F NKLV (Nef Xylem late wood vertical) Pinus taeda cDNA

DEFINITION AT5G47030 ATP synthase delta chain, mitochondrial precursor (sp|Q96252) see <http://mips.gsf.de/proj/thal/db/index.html>, mRNA sequence.

ACCESSION B0198462

VERSION B0198462.1 GI:20384424

KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)

ORGANISM Pinus taeda

REFERENCE 1 (bases 1 to 419)

AUTHORS Sederoff,R.

TITLE Molecular Basis of Wood Formation in the Pine Megagenome

JOURNAL Unpublished (2000)

COMMENT Contact: Sederoff, Ron

Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron_sederof@ncsu.edu, jerri_johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
information.
Seq primer: T3.

FEATURES
source
location/Qualifiers
1..419
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3152"
/clone="NX1V131.F01"
/tissue_type="primary xylem"
/dev_stage="late wood"
/lab_host="XLA-Blue"
/clone_lib="NX1V (Nef Xylem late wood Vertical)"
/note="Vector: pT7BlueX; Site 1: EcoRI; The library is
from late (summer-August) wood, taken from below the crown
of a 20 year old tree. The harvested xylem tissue was on
the cusp between transitional and mature wood. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATCGGCATATGCGC'."

ORIGIN
Query Match 93.8%; Score 15; DB 5; Length 419;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AAAGCCACCCAGGC 15
246 AAAGCCACCCAGGC 232

RESULT 36
AA147417 423 bp mRNA linear EST 06-AUG-1997
LOCUS 2399e07.r1 StrataGene endochelial cell 937223 Homo sapiens cDNA
DEFINITION clone IMAGE:589284 5' similar to gb:D13748 EUKARYOTIC INITIATION
FACTOR 4A-1 (HUMAN); mRNA sequence.
ACCESSION AA147417 GI:1716788
VERSION AA147417
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 423)
Haller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiselli, B.,
Chisese, S., Dietrich, N., Dubugue, T., Favello, A., Gish, N.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Roehling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevisan, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbl.gov) for further information.
Insert Length: 1549 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 304.
Location/Qualifiers
1..423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4627024"
/db_xref="taxon:9606"
/clone="IMAGE:589284"
/dev_stage="umbilical vein, 1 passage"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene endothelial cell 937223"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
umbilical vein endothelial cells, passaged once. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGGCGAG 3' ~3' adaptor sequence: 5'
CTCGAGCTTTTCTTTTCTTTTCTTTT 3'."

ORIGIN
Query Match 93.8%; Score 15; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AAAGCCACCCAGGC 15
284 AAAGCCACCCAGGC 298

RESULT 37
CN125873 448 bp mRNA linear EST 01-APR-2004
LOCUS RHOH1_13.G11.A002 Acid- and alkaline-treated roots Sorghum
DEFINITION bicolor cDNA clone RHOH1_13.G11.A002 5', mRNA sequence.
ACCESSION CN125873
VERSION CN125873.1 GI:45950664
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 448)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: acid- and alkaline-treated roots
Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpatr@cuga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
Location/Qualifiers
1..448
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="RHOH1_13.G11.A002"
/lab_host="PH10B-P1 Phage-resistant E. coli"
/clone_lib="Acid- and alkaline-treated roots"
/note="Organ: Root; Vector: pMB185-P13; Site 1: XhoI;

FEATURES
source
location/Qualifiers
1..448
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="RHOH1_13.G11.A002"
/lab_host="PH10B-P1 Phage-resistant E. coli"
/clone_lib="Acid- and alkaline-treated roots"
/note="Organ: Root; Vector: pMB185-P13; Site 1: XhoI;

Site 2: XhoI; The library was prepared from polyA+ RNA from 8-day-old roots harvested from Btx623 sorghum seedlings grown in hydroponic culture. HCl was added to a pH of 3.0 to some seedlings, KOH to a pH of 9.0 for others. Roots were harvested 3, 12 and 27 hr after addition and pooled for RNA preparation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCAGTGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 93.8%; Score 15; DB 7; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
|||||
Db 193 AAGCCACCCAGGCA 207

RESULT 38 455 bp mRNA linear EST 27-DEC-2002
CA902085 PCS04956 Scarlet Runner Bean Suspensor Region Triplex2 Phaseolus
LOCUS coccineus cDNA 5' similar to Nucleoid DNA-binding protein, mRNA
DEFINITION

ACCESSION CA902085 GI:27389077
VERSION EST.
KEYWORDS Phaseolus coccineus
SOURCE Phaseolus coccineus
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
1 (bases 1 to 455)
Bui, A.O., Le, B.H., Weeterings, K., Bi, Y.-P., Choi, D.-S.,
McElroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and
Goldberg, R.B.
Gene Activity in Different Regions of a Post-Fertilization Plant
Embryo by EST Analysis
Unpublished (2002)
Contact: Goldberg, R.B.
Department of Molecular, Cell, & Developmental Biology
University of California, Los Angeles
621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
Tel: 310 825 3270
Fax: 310 825 8201
Email: bobg@ucla.edu
Seq primer: 5' Triplex
POLYA=No.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1..455
/organism="Phaseolus coccineus"
/mol_type="mRNA"
/cultivar="Hammond's Dwarf Scarlet"
/db_xref="taxon:3886"
/dev_stage="6-days post-pollination"
/clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
/note="Organ: Suspensor Region of Globular-stage Embryos;
Vector: Triplex2; Site 1: SfiI; Site 2: SfiI; Suspensor
regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants
[Weeterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction kit according to
the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the SfiI restriction site
of the lambda Triplex2 vector (Clontech), and the
recombinant cDNAs were transformed into E. coli XL1-Blue
cells (Clontech). Suspensor cDNA plasmids used for
directional sequencing were obtained by in vivo excision

from the lambda Triplex2 recombinants in E. coli BM25.8
cells (Clontech)."

ORIGIN

Query Match 93.8%; Score 15; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCCACCCAGGCA 16
|||||
Db 201 AAGCCACCCAGGCA 215

RESULT 39 459 bp mRNA linear EST 27-JAN-1997
AA205003
LOCUS zq72e12.r1 Stragatene neuroepithelium (#937231) Homo sapiens cDNA
clone IMAGE:647182 5' similar to gp:DJ3748 EUKARYOTIC INITIATION
DEFINITION FACTOR 4A-1 (HUMAN);, mRNA sequence.
AA205003
AA205003.1 GI:1803035
EST.

ACCESSION AA205003
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 459)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
Chisone, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucada, F., Lacy, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rife, L.,
Rohlfing, T., Scheilenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevasaks, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 326.

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1..459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5217434"
/db_xref="taxon:9606"
/clone="IMAGE:647182"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stragatene neuroepithelium (#937231)"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2
cells (Ntera-2/Cl.D1) induced with Retinoic Acid for 24
hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATCGGACGCG 3' -3' adaptor
sequence: 5' CTCGAGTCTTTT TTTT TTTT 3'

ORIGIN

Query Match 93.8%; Score 15; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCACCCAGGCA 15
|||||
Db 285 AAGCCACCCAGGCA 299

```

RESULT 40
LOCUS B2180217/c 495 bp DNA linear GSS 11-OCT-2002
DEFINITION CH230-485E5.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION B2180217
VERSION B2180217
KEYWORDS CH230-485E5, genomic survey sequence.
SOURCE B2180217.1 GI:23824776
ORGANISM GSS.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 495)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,
Shivartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
COMMENT Other_GSSs: CH230-485E5.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). BAC end
page: http://www.tigr.org/tldb/bac\_ends/rat/bac\_end\_intro.html
Plate: 465 row: E column: 5
Seq primer: SP6
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..495
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHed/MCW"
/db_xref="taxon:10116"
/clone="CH230-485E5"
/sex="Female"
/cell_type="Brain"
/clone_id="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; site 2: MboI;
CHORI-230 Rat (BN/SsNHed/MCW) BAC library produced by
Pieter de Jong"
ORIGIN
Query Match 93.8%; Score 15; DB 8; Length 495;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAGCCACCCCAAGCA 16
DB 370 AAGCCACCCCAAGCA 356

```

Search completed: March 31, 2005, 14:44:31
 Job time : 1707 secs